

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:39:49 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAMPPTPL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	50.0	10	2 A36454	trypsin-modulating lectin - potato (F
2	24	44.4	8	2 S21288	urease (EC 3.5.1.5
3	21	38.9	10	2 C35389	peptide-N4-(N-acet
4	21	38.9	10	2 B59272	major protein anti
5	20	37.0	5	2 B60274	enamelin f - Bovin
6	20	37.0	8	2 S10783	T-cell receptor be
7	19	35.2	9	2 B30572	exotoxin A - Strep
8	19	35.2	9	2 A60108	collagen alpha 2(V
9	19	35.2	10	2 S26508	T-cell receptor be
10	19	35.2	10	2 C30572	metallothionein-A
11	18	33.3	4	2 IS1049	triacylglycerol 11
12	18	33.3	8	2 S71919	hemocytin (EC 3.4.-
13	18	33.3	10	2 PC2171	alpha-gliadin 4Ha
14	17	33.3	10	2 A61007	acid protease 11
15	17	31.5	10	2 A61218	ATPase K1 subunit
16	17	31.5	10	2 B61218	orf 1 para 5'-regi
17	16	29.6	5	2 B37988	granulocyte-colony
18	16	29.6	9	2 D48186	dissimulatory sulf
19	16	29.6	9	2 S15594	vitamin D3 26-mono
20	16	29.6	10	2 PH1633	probable methionin
21	15	27.8	8	4 IS4017	ig H chain V-D-J r
22	15	27.8	9	2 S63491	T-cell receptor be
23	15	27.8	9	2 S15850	probable glucose-6
24	15	27.8	10	2 B39517	triacylglycerol 11
25	15	27.8	10	2 PH1592	ig mu chain J regi
26	15	27.8	10	2 PT0664	
27	15	27.8	10	2 S18396	
28	15	27.8	10	2 PX0030	
29	15	27.8	10	2 F33932	

30	14	25.9	7	2 S71299
31	14	25.9	7	2 PT0283
32	14	25.9	7	2 A61081
33	14	25.9	8	2 B39745
34	14	25.9	8	2 S16324
35	14	25.9	8	2 PT0559
36	14	25.9	8	2 A23967
37	14	25.9	8	2 B47393
38	14	25.9	9	2 S35538
39	14	25.9	9	2 S65433
40	14	25.9	9	2 B41983
41	14	25.9	9	2 A43065
42	14	25.9	9	2 A26744
43	14	25.9	9	2 A61057
44	14	25.9	9	2 A60579
45	14	25.9	9	2 B60246

ALIGNMENTS

RESULT 1
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #ext_change 09-Jul-2004
C/Accession: A36454; A61630
R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A/Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme b
A/Reference number: A36454; PMID:90367888; PMID:2394318
A/Accession: A36454
A/Molecule type: protein
A/Residues: 1-10 <BOR>
A/Cross-references: UNIPROT:P19425
R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A/Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oos
A/Reference number: A61630; PMID:93357794; PMID:8353526
A/Accession: A61630
A/Molecule type: protein
A/Residues: 1-10 <BO2>
A/Note: none of the amino acids is modified
C/Function:
A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ei
C/Keywords: hormone

Query Match
Best Local Similarity 50.0%; Score 27; DB 2; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPPP 9
DB 2 DPAP 6

RESULT 2
S21288
lectin - potato (fragment)
C/Species: Solanum tuberosum (potato)
C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #ext_change 09-Jul-2004
C/Accession: S21288
R/Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A/Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati
A/Reference number: S21288; PMID:92272683; PMID:1590771
A/Accession: S21288
A/Molecule type: protein
A/Residues: 1-8 <MT>
A/Cross-references: UNIPROT:Q7M1V6
A/Experimental source: var. Ulster Sceptre
C/Function:
A/Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 44.4%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 AMDPPTP 9
| | | |
DB 2 ASTRPSP 8

RESULT 3

C35389

urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)

C;Species: Morganella morganii

C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004

C;Accession: C35389

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A;Title: Morganella morganii urease: purification, characterization, and isolation of ge

A;Reference number: A35389; PMID:90264298; PMID:2345135

A;Accession: C35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HNA>

A;Cross-references: UNIPROT:P17339

C;Keywords: hydrolase

Query Match 38.9%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 MDPTTP 9
| | | |
DB 1 MOUTTP 6

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
N;Alternate names: peptide-N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: B59272

R;Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998

A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A

A;Reference number: A59272; PMID:96181894; PMID:9525720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

A;Cross-references: UNIPROT:P81898

C;Keywords: hydrolase

Query Match 38.9%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 DPTP 8
| | | |
DB 1 BPTP 4

major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: B60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; PMID:9109989; PMID:1698899

A;Accession: B60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 37.0%; Score 20; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DPTP 8
| | | |
DB 1 DPAP 4

enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C;Accession: S10783

R;Strawich, E.; Glimcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu

A;Reference number: S10780; PMID:90336641; PMID:2379503

A;Accession: S10783

A;Molecule type: protein

A;Residues: 1-8 <STR>

C;Keywords: enamel; phosphoprotein

Query Match 37.0%; Score 20; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 PTPP 9
| | | |
DB 2 PLPP 5

T-cell receptor beta chain C region (CRTB29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997

C;Accession: B30572

R;Williams, C.B.; Gorman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; PMID:89110038; PMID:2563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <MTL>

C;Keywords: T-cell receptor

Query Match 35.2%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TPP 9
| | | |
DB 7 TPP 9

Streptococcus pyogenes (strain C203.S) (fragment)
N;Alternate names: blastogen A; scarlet fever toxin
C;Species: Streptococcus pyogenes

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 03-Jul-2004

C;Accession: A60108

R;Schliewert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

RESULT 14

A61007
 hementin (EC 3.4.-.-) - Amazon leech (fragment)
 C/Species: Haementeria ghilianii (Amazon leech)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: A61007
 R/Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
 J. Chromatogr. 502, 359-369, 1990
 A/Title: Purification and characterization of hementin, a fibrinogenolytic protease from
 A/Reference number: A61007; MUID:90256973; PMID:2187898
 A/Accession: A61007
 A/Molecule type: protein
 A/Residues: 1-10 <SMA>
 A/Cross-references: UNIPROT:Q7M3P9
 C/Keywords: anticoagulant; hydrolase; saliva

Query Match 33.3%; Score 18; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DPTPL 10
 :| | |
 Db 5 EPPDL 10

RESULT 15

A61218
 alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
 C/Species: Haynaldia villosa, Dasytrum villosum
 C/Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
 C/Accession: A61218
 R/Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
 Biochem. Genet. 29, 207-211, 1991
 A/Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald
 A/Reference number: A61218; MUID:91315394; PMID:1859356
 A/Accession: A61218
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <SHE>
 A/Cross-references: UNIPROT:Q7M1F7
 C/Keywords: seed; storage protein

Query Match 31.5%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 PTPPL 10
 :| | |
 Db 5 PVPOL 9

Search completed: January 6, 2005, 10:51:16
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:25:17 ; Search time 187 Seconds

(without alignments)
30.769 Million cell updates/sec

Title: US-10-047-945-1

Sequence: 1 LKMDPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	50.0	10	1	TMOP_AEDAE
2	24	44.4	8	2	Q7M1V6
3	23	42.6	10	2	Q76MK5
4	23	42.6	10	2	BAB87160
5	21	38.9	9	2	Q6SP94
6	21	38.9	9	2	Q99193
7	21	38.9	9	2	AAR20844
8	21	38.9	10	1	URE3_MORMO
9	21	38.9	10	2	P81898
10	20	37.0	7	1	UF04_MOUSE
11	20	37.0	10	2	Q91W23
12	20	37.0	10	2	Q75595
13	20	37.0	10	2	AAP76567
14	19	35.2	9	2	Q7M2M9
15	19	35.2	10	1	PAS_MACRS
16	19	35.2	10	1	UHA3_HUMAN
17	19	35.2	10	1	P90391
18	19	35.2	10	2	Q8JY66
19	19	35.2	10	2	Q8JY68
20	19	35.2	10	2	Q8JY70
21	19	35.2	10	2	Q8JY72
22	19	35.2	10	2	Q8JY74
23	19	35.2	10	2	Q8JY76
24	19	35.2	10	2	Q8JY78
25	19	35.2	10	2	Q8JY82
26	19	35.2	10	2	Q9Q0V7
27	19	35.2	10	2	Q9Q0V9
28	19	35.2	10	2	Q9Q0W1
29	19	35.2	10	2	Q9Q0W3
30	19	35.2	10	2	Q9Q0W5
31	19	35.2	10	2	Q9Q0W7

32	19	35.2	10	2	Q9Q0W9
33	19	35.2	10	2	Q9Q0X1
34	19	35.2	10	2	Q9Q0X3
35	19	35.2	10	2	Q9Q0X5
36	19	35.2	10	2	Q9Q0X9
37	18	33.3	8	2	Q6UN69
38	18	33.3	8	2	Q7L246
39	18	33.3	8	2	AAQ83766
40	18	33.3	8	2	AAQ83767
41	18	33.3	10	2	Q7M3P9
42	18	33.3	10	2	Q76MM1
43	18	33.3	10	2	Q9S905
44	18	33.3	10	2	Q8VHM9
45	18	33.3	10	2	Q84140

ALIGNMENTS

RESULT 1	TMOP_AEDAE	STANDARD;	PRT;	10 AA.
ID	P19425;			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Trypsin-modulating coelastatic factor (TMOP) (OOSH).			
OS	Aedes aegypti (Yellowfever mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.			
OX	NCBI_TaxId=7159;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=Vero beach; TISSUE=Ovary;			
RX	MEDLINE=93357794; PubMed=8353526;			
RA	Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;			
RT	"Mass spectrometry and characterization of Aedes aegypti trypsin			
RT	modulating coelastatic factor (TMOP) and its analogs.";			
RL	Insect Biochem. Mol. Biol. 23:703-712(1993).			
CC	-1- FUNCTION: Has an coelastatic activity. Inhibits trypsin biosynthesis			
CC	in the midgut which indirectly reduces the vitellogenin			
CC	concentration in the hemolymph resulting in inhibition of oocyte			
CC	development.			
CC	-1- DEVELOPMENTAL STAGE: Synthesized and released from follicular			
CC	epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs			
CC	and stops at 56 hrs.			
DR	PIR; A36454; A36454.			
FT	Direct protein sequencing; Hormone.			
FT	DOMAIN 3 10			
FT	VARIANT 1 2			
FT	YD -> DY (IN TMOP(B)).			
SO	SEQUENCE 10 AA; 1047 MW; 236DQA777776DC7 CRC64;			
Query Match	50.0%;	Score 27;	DB 1;	Length 10;
Best Local Similarity	80.0%;	Pred. No. 4.6e+02;		
Matches 4;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	5 DPFP 9			
Db	2 DPFP 6			
RESULT 2	Q7M1V6	PRELIMINARY;	PRT;	8 AA.
ID	Q7M1V6			
AC	Q7M1V6;			

DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE lectin (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NCBI_Taxid=4113;
 RN [1]
 RP SEQUENCE.
 RA Miller D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
 RA Bolwell G.P.;
 RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
 RT Characterization, immunolocalization and effects of wounding.";
 RL Biochem. J. 283:813-821(1992).
 DR PIR, S21288; S21288.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 771 MW; C37775A71B5BDA CRC64;

Query Match 44.4%; Score 24; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMPPTP 9
 Db 2 ASTPSP 8

RESULT 3
 Q76MK5 PRELIMINARY; PRT; 10 AA.
 AC Q76MK5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN Name=ATPase 8;
 OS Eurypharynx pelicanoides (pelican eel).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 NCBI_Taxid=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22967687; PubMed=12949142;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 RT scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 DR GO, GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 42.6%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
 Db 4 LDPSP 8

RESULT 4
 BAB87160

ID BAB87160 PRELIMINARY; PRT; 10 AA.
 AC BAB87160;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATPase 8.
 OS Eurypharynx pelicanoides (pelican eel).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 NCBI_Taxid=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
 RT Scale Gene Rearrangements Originated Within the Eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 DR EMBL, AB046487; BAB87160.1; -.
 KW Mitochondrion.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 42.6%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
 Db 4 LDPSP 8

RESULT 5
 Q6SP94 PRELIMINARY; PRT; 9 AA.
 AC Q6SP94;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE PF26 (Fragment).
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadales; Chlamydomonas.
 NCBI_Taxid=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CC-2290;
 RX MEDLINE=22570934; PubMed=12684385;
 RA Kachir P., Lavole M., Brazelton W.J., Haas N.A., Lefebvre P.A.,
 RA Silflow C.D.;
 RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
 RL Eukaryotic Cell 2:362-379(2003).
 DR EMBL, AY454155; AAR20844.1; -.
 KW Non TER 1
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;

Query Match 38.9%; Score 21; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTTP 9
 Db 1 PAPP 4

RESULT 6

```

099193
ID 099193; PRELIMINARY; PRT; 9 AA.
AC 099193;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RpoB beta-subunit of RNA polymerase (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
[1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sveridov D.;
RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RT RNA polymerase in Pseudomonas putida."
RL Dokl. Biochem. 302:1261-1265(1998).
DR EMBL; X15849; CAA33847.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 852 MW; SB416776DC76727 CRC64;

Query Match 38.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
DB 4 PAPP 7

RESULT 7
AAR20844 PRELIMINARY; PRT; 9 AA.
ID AAR20844;
AC AAR20844;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE PF26 (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=CC-2290;
RX MEDLINE=22570934; PubMed=12684385;
RA Kathir P., Lavole M., Brazelton W.J., Haas N.A., Lefebvre P.A.,
RA Silflow C.D.;
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome."
RL Eukaryotic cell 2:362-379(2003).
DR EMBL; AY454155; AAR20844.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1012 MW; DB0AAB1B07776D CRC64;

Query Match 38.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
DB 1 PAPP 4

RESULT 8
URR3 MORMO STANDARD; PRT; 10 AA.
ID URR3 MORMO
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
DE (Urease 6 kDa subunit) (Fragment).

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GN Name=urea;
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
[1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences."
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the urease gamma subunit family.
DR PIR; C35389; C35389.
DR HAMAP; MF 00739; -; 1.
KW Direct protein sequencing; Hydrolase.
FT NON_TER
SQ SEQUENCE 10 AA; 1171 MW; 4B13BCB077771A7 CRC64;

Query Match 38.9%; Score 21; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
DB 1 MOLTTP 6

RESULT 9
P81898 PRELIMINARY; PRT; 10 AA.
ID P81898;
AC P81898;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, small
DE chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
[1]
RP SEQUENCE AND CHARACTERIZATION.
RX PubMed=9523720.
RA Altman F., Paschinger K., Dalk T., Vorauer K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT amidase A and its N-glycans."
RL Eur. J. Biochem. 252:118-123(1998).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -1- MASS SPECTROMETRY: MW=21247; METHOD=MALDI.
DR PIR; B59272; B59272.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000224; F:peptide-N4-(N-acetyl-beta-glucosaminyl) aspa. .; IEA.
KW Glycoprotein; Hydrolase.
FT NON_TER
SQ SEQUENCE 10 AA; 1149 MW; 863278CA1B73771 CRC64;

Query Match 38.9%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 DPTP 8
: |||
Db 1 EPTP 4

RESULT 10
ID UP04 MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.,
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 46 kDa.
KM Direct protein sequencing.
FT NON_TER
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 37.0%; Score 20; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
: |||
Db 1 PKPP 4

RESULT 11
ID Q91W23 PRELIMINARY; PRT; 10 AA.
AC Q91W23;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen O.X., Liu H.H., Chen W.Y., Bahl O.P.,
RT "Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells.";
RL Acta Biol. Exp. Sinica 28:283-290(1995).
DR EMBL, S80660; AAB50710.1; -.
DR GO; GO:004872; P:receptor activity; IBA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .); IBA.
KM Chorion Receptor.
FT NON_TER
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC417760 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9

Db 2 PTPP 5
: |||
1 MEPVDP 6

RESULT 12
ID Q75595 PRELIMINARY; PRT; 10 AA.
AC Q75595;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Tat protein (fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.,
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57303; AAB17863.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1182 MW; 22252B34176AB2D7 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTP 9
: |||
Db 1 MEPVDP 6

RESULT 13
ID AAP76567 PRELIMINARY; PRT; 10 AA.
AC AAP76567;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Truncated tat protein.
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=99ET8;
RA Harris M.E., Maayan S., Kim B., Zelra M., Ferrari G., Birx D.L.,
RT "A cluster of HIV type 1 subtype C sequences from Ethiopia, observed
RT in full genome analysis, is not substituted in subgenomic regions.";
RL AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=99ET8;
RA Harris M.E., Birx D.L.,
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=99ET8;
RA Maayan S., Zelra M.,
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY255828; AAP76567.1; -.
SQ SEQUENCE 10 AA; 1154 MW; 22252E3276AB2D7 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
DB 1 MERVDP 6

RESULT 14

Q7M2M9 PRELIMINARY; PRT; 9 AA.
AC Q7M2M9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Collagen alpha 2 (VI) chain (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.

RX MEDLINE=83209648; PubMed=6852033;
RA Jander R., Raubenberg J., Gnanville R.W.;
RT "Further characterization of the three polypeptide chains of bovine
and human short-chain collagen (intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26508; S26508.
FT NON_TER 1 1
FT NON_TER 9 9

SQ SEQUENCE 9 AA; 876 MW; 68146776867605B CRC64;

Query Match 35.2%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTTP 9
DB 4 PGPP 7

RESULT 15

PAR5_MACRS STANDARD; PRT; 10 AA.
ID PAR5_MACRS
AC P83278;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE FMRamide-like neuropeptide PLPS (DRTPALRLR-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_Taxid=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RA TISSUE=Eyestalk;
RC Stihgornngul P., Sarathongkum W., Jaidechoe S., Longant S.,
RA Stihgornngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI; RANGE=1-10;
CC NOTB=Ref.1.

CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.

DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC771 CRC64;

Query Match 35.2%; Score 19; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DPTPL 10
DB 1 DRTPAL 6

Search completed: January 6, 2005, 10:50:32
Job time : 189 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:23:57 ; Search time 149 Seconds
(without alignments)
24.076 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPDTPPL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq.23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	2	AAW53843
2	54	100.0	10	7	ABB80222
3	50	92.6	9	7	ABB80227
4	43	79.6	8	7	ABB80228
5	30	55.6	6	4	AA66473
6	30	55.6	6	5	ABB78481
7	30	55.6	10	5	ABB78478
8	28	51.9	9	2	AAV7988
9	28	51.9	9	3	AAV6825
10	28	51.9	9	3	AAV6825
11	28	51.9	9	8	ADK07609
12	28	51.9	10	2	AA61547
13	28	51.9	10	2	AA61547
14	28	51.9	10	2	AAV48003
15	28	51.9	10	8	ADK07609
16	27	50.0	6	2	AA63465
17	27	50.0	6	2	AA63465
18	27	50.0	6	2	AA63465
19	27	50.0	6	2	AA63465
20	27	50.0	6	2	AA63465
21	27	50.0	6	3	AA63465
22	27	50.0	6	4	AA63465
23	27	50.0	6	6	ABP58325
24	27	50.0	6	7	ADC35474
25	27	50.0	6	7	ADD10251

26	27	50.0	7	2	AA656875	AA656875 Oostatic
27	27	50.0	7	2	AA63466	AA63466 Trypsin M
28	27	50.0	7	2	AA63466	AA63466 Trypsin M
29	27	50.0	7	2	AA63466	AA63466 Trypsin M
30	27	50.0	7	2	AA63466	AA63466 Trypsin M
31	27	50.0	7	3	AA63466	AA63466 Trypsin M
32	27	50.0	7	4	AA63466	AA63466 Trypsin M
33	27	50.0	7	6	ABP58326	ABP58326 Trypsin m
34	27	50.0	7	7	ADC35475	ADC35475 Trypsin m
35	27	50.0	7	7	ADD10252	ADD10252 Mosquito
36	27	50.0	8	2	AA656873	AA656873 Oostatic
37	27	50.0	8	2	AA63467	AA63467 Trypsin M
38	27	50.0	8	2	AA63467	AA63467 Trypsin M
39	27	50.0	8	2	AA63467	AA63467 Trypsin M
40	27	50.0	8	2	AA63467	AA63467 Trypsin M
41	27	50.0	8	2	AA63467	AA63467 Trypsin M
42	27	50.0	8	3	AA63467	AA63467 Trypsin m
43	27	50.0	8	4	AA63467	AA63467 Trypsin m
44	27	50.0	8	6	ABP58327	ABP58327 Trypsin m
45	27	50.0	8	7	ADC35476	ADC35476 Trypsin m

ALIGNMENTS

RESULT 1					
ID	AAW53843	standard; peptide; 10 AA.			
AC	AAW53843;				
XX					
XX					
DT	08-UTL-1998 (first entry)				
XX					
DE	N-terminus of opoosum LTNP.				
XX					
KW	LTNP; lethal toxin neutralising factor; opoosum; envenomation; therapy;				
KW	anti-haemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite;				
KW	sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;				
KW	histamine reaction treatment.				
OS	Didelphis virginiana.				
XX					
PN	US5744449-A.				
XX					
PD	28-APR-1998.				
XX					
PP	03-JUN-1996; 96US-00657163.				
XX					
PR	10-MAY-1993; 93US-00058387.				
XX					
PR	22-SEP-1994; 94US-00310340.				
XX					
PA	(LIPF/) LIPPS B V.				
XX	(LIPF/) LIPPS F W.				
PI	Lipps FW, Lipps BV;				
XX					
DR	WPI; 1998-271108/24.				
XX					
PT	Lethal Toxin Neutralising Factor peptide from opoosum - can neutralise				
XX	venom(s) from all major families of poisonous snakes.				
PS	Claim 7, Col 11; lipp; English.				
XX					
CC	This sequence represents the peptide of the invention. It is a lethal				
CC	Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic				
CC	protein derived from an opoosum. The peptide can be used in a method for				
CC	treating a victim of envenomation from a poisonous snake, preferably a				
CC	poisonous snake from the family of Elapidae, Viperidae or sea snake. It				
CC	is useful for the treatment of snake bites, sepsis, allergies caused by				
CC	the environment and treatment of bee or scorpion stings or toxicities				
CC	caused by plant or bacterial toxins. The peptide can also be used in				
CC	histamine reaction treatment. The peptide can be used in envenomation				
CC	treatment for a variety of snakes without prior identification of the				

CC snake. Being short it can be synthetically prepared rather than the
CC current production in horses, where some people can show hypersensitivity
CC to horse proteins

XX Sequence 10 AA;

Query Match 100.0%; Score 54; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
| | | | | | | | | |
Db 1 LKAMDPTPPL 10

RESULT 2
ABB80222
ID ABB80222 standard; peptide; 10 AA.

XX ABB80222;

DT 06-NOV-2003 (first entry)

XX Synthetic LTNF, LT-10.

DE Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.

XX Synthetic.

PN W02003060471-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001044.

XX 14-JAN-2002; 2002US-00047945.

XX (LIPF/) LIPPS B V.
PA (LIPF/) LIPPS F W.

XX LIPPS BV, LIPPS FW;

XX WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.

XX Claim 7; Page 3; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin B (IGB), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGF levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA

XX Sequence 10 AA;

Query Match 100.0%; Score 54; DB 7; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
| | | | | | | | | |
Db 1 LKAMDPTPPL 10

RESULT 3
ABB80227
ID ABB80227 standard; peptide; 9 AA.

XX ABB80227;

DT 06-NOV-2003 (first entry)

XX Synthetic LTNF, LT-9.

DE Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.

XX Synthetic.

PN W02003060471-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001044.

XX 14-JAN-2002; 2002US-00047945.

XX (LIPF/) LIPPS B V.
PA (LIPF/) LIPPS F W.

XX LIPPS BV, LIPPS FW;

XX WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.

XX Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin B (IGB), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGF levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA

XX Sequence 9 AA;

Query Match 92.6%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 9
 |||||
 1 LKAMDPTP 9

RESULT 4

ABB80228 standard; peptide; 8 AA.

AC ABB80228;
 DT 06-NOV-2003 (first entry)
 XX Synthetic LTNF, LT-8.
 DE

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KM IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM salivA; ELISA.

XX Synthetic.

OS WO2003060471-A2.

PN 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

XX (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.

XX Lippe BV, Lippe FW;

XX WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a salivA sample from a
 PT patient.
 XX

PS Claim 7, Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGB), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a salivA
 CC sample using an anti-serum that is specific for the protein. SalivA
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. SalivA can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. SalivA proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

Query Match 79.6%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
 |||||
 1 LKAMDPTP 8

RESULT 5

ABB68473 standard; peptide; 6 AA.

AC AAB68473;
 DT 23-JUL-2001 (first entry)
 XX

XX Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
 DE Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin;
 KM chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
 XX

OS Synthetic.

OS Saccharomyces paradoxus.

PN US6228647-B1.

XX 08-MAY-2001.

PF 15-JAN-1999; 9US-00232446.

PR 15-JAN-1998; 9US-0071383P.

PA (IOWA) UNIV IOWA STATE RES FOUND INC.

XX Voytas DF, Gal X;

XX WPI; 2001-342676/36.

PT Targeting integration of retrotransposon or retrovirus into silent
 PT chromatin by transforming a cell with modified integrase having a coding
 PT sequence for a peptide portion that interacts with chromatin at desired
 PT sites.
 XX

PS Claim 13; Col 66; 41pp; English.

XX The present sequence represents a mutated portion of an integrase. The
 CC specification describes a method for targeting integration of
 CC retrotransposon of Ty1-copia group to desired location on a chromosome.
 CC The method uses a modified integrase in a retrotransposon, where the
 CC modified integrase contains a coding sequence for a peptide portion which
 CC specifically binds to protein bound to the chromosome or to particular
 CC nucleic acid sequences on chromosome. The method is useful for targeting
 CC integration of a retrotransposon of the Ty1-copia group to a desired
 CC location on a chromosome, especially into silent chromatin. The silent
 CC chromatin targeting of Ty5 is useful for tagging genes which are affected
 CC by aging and for studying oncogenes

XX Sequence 6 AA;

Query Match 55.6%; Score 30; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 9
 :||:|
 1 LDPSPP 6

RESULT 6

ABB78481 standard; peptide; 8 AA.

XX ABB78481;
 DT 09-JUL-2002 (first entry)

XX Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:168.
 DE
 XX
 KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
 KM HRP; repetitive proline-rich protein; RRP; arabinogalactan protein;
 XX AGP; plant gum.
 XX
 OS Acacia senegal.
 OS Synthetic.
 XX
 PN WO200178503-A2.
 PD
 XX 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US012336.
 XX
 PR 12-APR-2000; 2000US-00547693.
 XX
 PA (UYOH-) UNIV OHIO.
 XX
 PI Kiejzowski MJ;
 XX
 DR WPI; 2002-041307/05.
 XX
 PT Nucleic acids and proteins useful for producing hydroxy-proline rich
 PT glycoproteins in plants.
 XX
 PS Claim 5; Page 121; 326pp; English.
 XX
 CC The present invention describes synthetic genes encoding plant gums and
 CC other hydroxyproline (Hyp)-rich glycoproteins (HRGs) and the nucleic
 CC acids that encode them. The nucleic acids, proteins and methods from the
 CC present invention may be used to produce HRP, repetitive proline-rich
 CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via
 CC recombinant methodologies. Also described is the expression of synthetic
 CC genes designed from repetitive peptide sequences, such as glycoproteins
 CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
 CC AB51730 to AB51849 and ABB78401 to ABB78544 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 8 AA;
 Query Match 55.6%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PTPPL 10
 DB 1 PTPPL 5
 RESULT 7
 ABB78478
 ID ABB78478 standard; peptide; 10 AA.
 AC
 XX ABB78478;
 DT
 XX 09-JUL-2002 (first entry)
 DE Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:165.
 KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
 KM HRP; repetitive proline-rich protein; RRP; arabinogalactan protein;
 XX AGP; plant gum.
 XX
 OS Acacia senegal.
 OS Synthetic.
 XX
 PN WO200178503-A2.
 PD
 XX 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US012336.

XX
 PR 12-APR-2000; 2000US-00547693.
 XX
 PA (UYOH-) UNIV OHIO.
 XX
 PI Kiejzowski MJ;
 XX
 DR WPI; 2002-041307/05.
 XX
 PT Nucleic acids and proteins useful for producing hydroxy-proline rich
 PT glycoproteins in plants.
 XX
 PS Claim 5; Page 121; 326pp; English.
 XX
 CC The present invention describes synthetic genes encoding plant gums and
 CC other hydroxyproline (Hyp)-rich glycoproteins (HRGs) and the nucleic
 CC acids that encode them. The nucleic acids, proteins and methods from the
 CC present invention may be used to produce HRP, repetitive proline-rich
 CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via
 CC recombinant methodologies. Also described is the expression of synthetic
 CC genes designed from repetitive peptide sequences, such as glycoproteins
 CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
 CC AB51730 to AB51849 and ABB78401 to ABB78544 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 10 AA;
 Query Match 55.6%; Score 30; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PTPPL 10
 DB 3 PTPPL 7
 RESULT 8
 AAY47988
 ID AAY47988 standard; peptide; 9 AA.
 AC
 XX AAY47988;
 DT
 XX 01-DEC-1999 (first entry)
 DE Immunogenic peptide having a human leukocyte antigen binding motif #2599.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW Immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 PD
 XX 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US005039.
 XX
 PR 13-MAR-1998; 98WO-US005039.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX
 DR WPI; 1999-551214/46.
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX
 PS Claim 1; Page 131; 150pp; English.

XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPTPL 10
 |||||
 Db 1 DPTPTPL 6

RESULT 9
 AAY6825

ID AAY6825 standard; peptide; 9 AA.

XX AC AAY6825;

XX DT 05-MAY-2000 (first entry)

XX DE Telomerase peptide #240.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;

XX KM malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;

XX OS telomerase T lymphocyte.

XX PN Homo sapiens.

XX PD WO200002581-A1.

XX PF 20-JAN-2000.

XX PR 30-JUN-1999; 99WO-NO000220.

XX PX 08-JUL-1998; 98NO-00003141.

XX PA (NHYD) NORSE HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

XX PI Saeboe-Larsen S;

XX DR WPI; 2000-145727/13.

XX PT Protein or peptide fragments useful in the treatment and prophylaxis of

XX PT cancer in mammals.

XX PS Claim 12; Page 36; 53pp; English.

CC This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or

CC pancreatic cancer, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal, with the
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence, T
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 3; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.7e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KANDPTPTPL 10
 :|||:
 Db 1 RAQDPTPTPL 9

RESULT 10
 AAY6735

ID AAY6735 standard; peptide; 9 AA.

XX AC AAY6735;

XX DT 05-MAY-2000 (first entry)

XX DE Telomerase peptide #150.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;

XX KM malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;

XX OS telomerase T lymphocyte.

XX PN Homo sapiens.

XX PD WO200002581-A1.

XX PF 20-JAN-2000.

XX PR 30-JUN-1999; 99WO-NO000220.

XX PX 08-JUL-1998; 98NO-00003141.

XX PA (NHYD) NORSE HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

XX PI Saeboe-Larsen S;

XX DR WPI; 2000-145727/13.

XX PT Protein or peptide fragments useful in the treatment and prophylaxis of

XX PT cancer in mammals.

XX PS Claim 12; Page 35; 53pp; English.

CC This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer. The
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancer, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal,
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells. Note: This sequence was indexed from WO200002581, which is the
 CC first major country equivalent to NO9803141

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 3; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
 :| | | |
 Db 1 RAODPPPEL 9

RESULT 11
 ADK07609
 ID ADK07609 standard; peptide; 9 AA.
 XX
 AC ADK07609;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hepatitis C virus CTL epitope peptide #5439.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KM virucide; vaccine; therapeutic agent; infection; epitope peptide;
 KM HLA-allele; CTL.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 XX
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTB-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR WPI; 2004-169243/16.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 14; Page 162; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the
 CC invention.
 CC
 SQ Sequence 9 AA;
 XX

Query Match 51.9%; Score 28; DB 8; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
 :| | | |
 Db 4 PTPPM 8

RESULT 12
 AAR61547
 ID AAR61547 standard; peptide; 10 AA.
 XX
 AC AAR61547;
 XX
 DT 25-MAR-2003 (revised)

DT 11-MAY-1995 (first entry)
 XX
 XX Peptide fragment (1.0507) of HCV binds HLA-A2.1.
 DE
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVb; EBV; HTLV;
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
 KW melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 5mer;
 KW 1mer; anchor; human leukocyte antigen.
 KM
 XX
 OS Hepatitis C virus.
 XX
 PN WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 04-MAR-1994; 94WO-US002353.
 XX
 PR 05-MAR-1993; 93US-00027146.
 XX
 PR 04-JUN-1993; 93US-00073205.
 XX
 PR 29-NOV-1993; 93US-00159184.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Sette A, Sidney J, Kast W;
 XX
 DR WPI; 1994-302678/37.
 XX
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
 PT treatment or prophylaxis of cancer, virus infection or autoimmune
 PT diseases.
 XX
 PS Example 5; Page 109; 138pp; English.
 XX
 CC AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR61547
 CC has an ICSO of 0.0042 and the sequence occurs at position 2803 in the HCV
 CC LORF protein. The peptides of the invention can induce cytotoxic T
 CC lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 10 AA;
 XX

Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DTPPPL 10
 :| | | |
 Db 5 DTPPL 10

RESULT 13
 AAR93336
 ID AAR93336 standard; peptide; 10 AA.
 XX
 AC AAR93336;
 XX
 DT 24-APR-1996 (first entry)
 XX
 DE YES protein tyrosine kinase derived peptide #9.
 XX
 KW SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; reestenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukemia; cancer.
 XX
 OS Synthetic.
 XX

PN MO9524419-A1.
 XX 14-SEP-1995.
 XX
 XX 13-MAR-1995; 95WO-US003208.
 XX
 PR 11-MAR-1994; 94US-00209835.
 PR 06-JAN-1995; 95US-00369832.
 XX
 PA (ARIA-) ARIAD PHARM INC.
 XX
 PI Rickles RJ, Brugge JS, Botfield MC, Zoller MJ;
 XX
 DR MPI, 1995-328231/42.
 PT Identification of peptide(s) binding specifically to SH3 domains - for
 PT use in inhibiting interactions mediated by SH3 domains in treatment of
 PT e.g. osteoporosis and cancer.
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC The sequences given in AAR93272-342 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library which
 CC comprises six random amino acids flanking the tetrapeptide -PIIP which
 CC was identified as a recognition sequence for the src SH3 domain. These
 CC sequences were identified using the method of the invention. The method
 CC comprises contacting the SH3 domain with a mixture of peptides under
 CC conditions permitting a ligand to bind to an SH3 domain to form a
 CC complex. Any unbound peptides are removed and the selected peptides are
 CC ligands are dissociated from the complexes. The selected peptides are
 CC enriched by re-contacting them with the SH3 domain and then candidates
 CC which bind to the SH3 domain are detected. The isolated SH3 binding
 CC peptides may be used in the diagnosis, prevention and treatment of
 CC conditions or diseases resulting from cellular processes mediated by an
 CC SH3-based interaction. Such diseases include Paget's disease. Other
 CC conditions treatable with these peptides include restenosis, rheumatoid
 CC arthritis, gout and other problems in which an SH3 of neutrophil oxidase
 CC p47 and p67 complex is implicated, etc
 CC
 SO Sequence 10 AA;
 XX
 QY Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 DB 2 KAMDPTPTPL 10
 1 KAKRPPLPI 9
 XX
 RESULT 14
 AAY48003
 ID AAY48003 standard; peptide; 10 AA.
 XX
 AC AAY48003;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #2614.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO945954-A1.
 XX
 PD 16-SBP-1999.
 XX

PF 13-MAR-1998; 98WO-US005039.
 XX
 XX 13-MAR-1998; 98WO-US005039.
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
 XX
 XX MPI, 1999-551214/46.
 DR
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX
 PS Claim 1; Page 132; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polypeptides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 CC
 SO Sequence 10 AA;
 XX
 QY Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 5 DPTPTPL 10
 1 DPTPTPL 6
 XX
 RESULT 15
 ADE97778
 ID ADE97778 standard; peptide; 10 AA.
 XX
 AC ADE97778;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Immunogenic HLA-A2.1 binding peptide #260.
 XX
 KW cytotoxic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotoxic; neuroprotective; antitachycardic; antineumatic;
 KW immunosuppressive; dermatological; muscular; nephrotoxic; thyromimetic;
 KW haemostatic; antihypertoid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.

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XX OS Synthetic.
XX PN US2003165822-A1.
XX PD 02-OCT-2003.
XX PF 03-APR-2002; 2002US-00116557.
XX PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
PR 02-DEC-1994; 94US-00349177.
XX PA (GREY/) GREY H M.
PA (SETT/) SETTE A.
PA (SIDN/) SIDNEY J.
XX PI Grey HM, Sette A, Sidney J;
XX PI WPI; 2004-041166/04.
XX DR
XX PT Immunogenic peptide composition for preventing, treating or diagnosing
PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved
PT residues at specified positions.
XX PS
XX PS Example 11; Page 25; 38pp; English.
XX CC The invention describes an immunogenic peptide composition comprising 9
CC residues including a first conserved residue at a second position from N-
CC terminus, and a second conserved residue at C-terminal position. The
CC inventive peptide composition is used to elicit an immune response
CC against a desired antigen for preventing, treating or diagnosing
CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune
CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
CC purpura, Grave's disease, and Addison's disease. The invention defines
CC positions within a motif enabling the selection of the peptides, which
CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
XX SQ
XX SQ Sequence 10 AA;
XX
XX Query Match 51.9%; Score 28; DB 8; Length 10;
XX Best Local Similarity 83.3%; Pred. No. 5.4e+02;
XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 DPTTPL 10
DB 5 DPTTPL 10

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Search completed: January 6, 2005, 10:47:18
 Job time : 151 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 10:50:39 ; Search time 141 Seconds
(without alignments)
25.572 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 183704

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	14	US-10-047-945-1
2	50	92.6	9	14	US-10-047-945-6
3	43	79.6	8	14	US-10-047-945-7
4	30	55.6	8	15	US-10-437-708-168
5	30	55.6	8	17	US-10-257-199-168
6	30	55.6	10	15	US-10-437-708-165
7	30	55.6	10	17	US-10-257-199-165
8	28	51.9	9	8	US-08-344-824-273
9	28	51.9	10	8	US-08-344-824-273
10	27	50.0	8	9	US-09-758-128-20
11	27	50.0	8	9	US-09-758-128-23
12	27	50.0	8	9	US-09-758-128-26
13	27	50.0	8	9	US-09-758-128-29

14	27	50.0	8	9	US-09-758-426-20	Sequence 20, Appl
15	27	50.0	8	9	US-09-758-426-23	Sequence 23, Appl
16	27	50.0	8	9	US-09-758-426-26	Sequence 26, Appl
17	27	50.0	8	9	US-09-758-426-29	Sequence 29, Appl
18	27	50.0	8	9	US-09-758-198-20	Sequence 20, Appl
19	27	50.0	8	9	US-09-758-198-23	Sequence 23, Appl
20	27	50.0	8	9	US-09-758-198-26	Sequence 26, Appl
21	27	50.0	8	9	US-09-758-198-29	Sequence 29, Appl
22	27	50.0	8	10	US-09-861-661-20	Sequence 20, Appl
23	27	50.0	8	10	US-09-861-661-23	Sequence 23, Appl
24	27	50.0	8	10	US-09-861-661-26	Sequence 26, Appl
25	27	50.0	8	10	US-09-861-661-29	Sequence 29, Appl
26	27	50.0	9	10	US-09-935-430-7	Sequence 7, Appl
27	27	50.0	9	14	US-10-224-999A-1613	Sequence 1613, Ap
28	27	50.0	9	14	US-10-277-232-7	Sequence 7, Appl
29	27	50.0	9	14	US-10-280-340-7	Sequence 7, Appl
30	27	50.0	9	15	US-10-149-138-2002	Sequence 2002, Ap
31	27	50.0	9	15	US-10-149-138-4046	Sequence 4046, Ap
32	27	50.0	9	15	US-10-149-138-4046	Sequence 4046, Ap
33	27	50.0	9	15	US-10-149-138-4159	Sequence 4159, Ap
34	27	50.0	9	15	US-10-398-104-47	Sequence 47, Appl
35	27	50.0	9	16	US-10-149-138-2002	Sequence 2002, Ap
36	27	50.0	9	16	US-10-149-138-4046	Sequence 4046, Ap
37	27	50.0	9	16	US-10-149-138-4159	Sequence 4159, Ap
38	27	50.0	10	10	US-09-935-430-74	Sequence 74, Appl
39	27	50.0	10	14	US-10-224-999A-1619	Sequence 1619, Ap
40	27	50.0	10	14	US-10-224-999A-1620	Sequence 1620, Ap
41	27	50.0	10	14	US-10-277-292-74	Sequence 74, Appl
42	27	50.0	10	14	US-10-277-292-619	Sequence 619, Appl
43	27	50.0	10	14	US-10-280-340-74	Sequence 74, Appl
44	27	50.0	10	14	US-10-280-340-619	Sequence 619, Appl
45	27	50.0	10	15	US-10-149-138-1347	Sequence 1347, Ap

ALIGNMENTS

RESULT 1
US-10-047-945-1
Sequence 1, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BIRIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN B
FILE REFERENCE: FWLPT015US
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
TYPE: PRT.
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OROSSUM
US-10-047-945-1

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMPPTPL 10
Db 1 LKAMPPTPL 10

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RESULT 2
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIIPS, BINIE V.
; APPLICANT: LIIPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match      92.6%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMDPTP 9
        |||||
Db      1 LKAMDPTP 9

RESULT 3
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIIPS, BINIE V.
; APPLICANT: LIIPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match      79.6%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
        |||||
Db      1 LKAMDPTP 8

RESULT 4
US-10-437-708-168
; Sequence 168, Application US/10437708
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; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-168

Query Match      55.6%; Score 30; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PTPL 10
        |||||
Db      1 PTPL 5

RESULT 5
US-10-257-199-168
; Sequence 168, Application US/10257199
; Publication No. US20040230032A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-06319
; CURRENT APPLICATION NUMBER: US/10/257,199
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-257-199-168

Query Match      55.6%; Score 30; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 PTPPL 10
|||||
Db 1 PTPPL 5

RESULT 6

US-10-437-708-165
; Sequence 165, Application US/10437708
; Publication No. US2004009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieleszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-165

Query Match 55.6%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
|||||
Db 3 PTPPL 7

RESULT 7

US-10-257-199-165
; Sequence 165, Application US/10257199
; Publication No. US20040230032A1
; GENERAL INFORMATION:
; APPLICANT: Kieleszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-06319
; CURRENT APPLICATION NUMBER: US/10/257,199
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE

QY 5 DPTPL 10
|||||
Db 1 DPTPL 6

LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-257-199-165

Query Match 55.6%; Score 30; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
|||||
Db 3 PTPPL 7

RESULT 8

US-08-344-824-273
; Sequence 273, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Baslian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA
US-08-344-824-273

Query Match 51.9%; Score 28; DB 8; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPL 10
|||||
Db 1 DPTPL 6

RESULT 9

US-08-344-824-381
; Sequence 381, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Stewart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-381

Query Match 51.9%; Score 28; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPL 10
DB 1 DPTPL 6

RESULT 10
US-09-758-128-20
; Sequence 20, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bovine
US-09-758-128-20

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPTPL 8

RESULT 11
US-09-758-128-23
; Sequence 23, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Porcine
US-09-758-128-23

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPTPL 8

RESULT 12
US-09-758-128-26
; Sequence 26, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 8
; TYPE: PRT

ORGANISM: Mouse
US-09-758-128-26

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPPL 8

RESULT 13
US-09-758-128-29
Sequence 29; Application US/09758128
Patent No. US20020107187A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187A1man L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,128
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 8
TYPE: PRT
ORGANISM: Rat
US-09-758-128-29

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPPL 8

RESULT 14
US-09-758-426-20
Sequence 20; Application US/09758426
Patent No. US20020169116A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116A1man L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Bovine
US-09-758-426-20

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPPL 8

RESULT 15
US-09-758-426-23
Sequence 23; Application US/09758426
Patent No. US20020169116A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116A1man L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,426
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 8
TYPE: PRT
ORGANISM: Porcine
US-09-758-426-23

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 1 AISPPL 8

Search completed: January 6, 2005, 11:02:39
Job time : 142 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:40:33 : Search time 37 Seconds
(without alignments)
17,924 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	1	US-08-657-163A-2
2	30	55.6	6	3	US-09-232-446B-24
3	30	55.6	8	4	US-09-547-693-168
4	30	55.6	10	4	US-09-547-693-165
5	27	50.0	6	1	US-07-989-290-2
6	27	50.0	6	1	US-08-271-698-2
7	27	50.0	6	1	US-08-468-596-2
8	27	50.0	6	4	US-09-295-996B-12
9	27	50.0	6	4	US-09-295-846B-15
10	27	50.0	6	4	US-09-551-737C-15
11	27	50.0	6	4	US-09-295-924B-2
12	27	50.0	7	4	US-09-551-738B-12
13	27	50.0	7	1	US-07-989-290-3
14	27	50.0	7	1	US-08-271-698-3
15	27	50.0	7	1	US-08-468-596-3
16	27	50.0	7	4	US-09-295-896B-13
17	27	50.0	7	4	US-09-295-846B-16
18	27	50.0	7	4	US-09-551-737C-16
19	27	50.0	7	4	US-09-295-924B-3
20	27	50.0	7	4	US-09-551-738B-13
21	27	50.0	8	1	US-07-989-290-4
22	27	50.0	8	1	US-08-271-698-4
23	27	50.0	8	1	US-08-468-596-4
24	27	50.0	8	4	US-09-295-996B-14
25	27	50.0	8	4	US-09-295-846B-17
26	27	50.0	8	4	US-09-551-737C-17
27	50.0		8	4	US-09-295-924B-4

28	27	50.0	8	4	US-09-551-738B-14	Sequence 14, Appl
29	27	50.0	10	4	US-09-295-996B-8	Sequence 8, Appl
30	27	50.0	10	4	US-09-295-846B-11	Sequence 11, Appl
31	27	50.0	10	4	US-09-551-737C-11	Sequence 11, Appl
32	27	50.0	10	4	US-09-295-924B-7	Sequence 7, Appl
33	27	50.0	10	4	US-09-551-738B-8	Sequence 8, Appl
34	26	48.1	4	3	US-08-895-590-40	Sequence 40, Appl
35	26	48.1	6	3	US-08-441-943-33	Sequence 33, Appl
36	26	48.1	6	4	US-08-897-556A-103	Sequence 103, App
37	26	48.1	7	4	US-09-641-803-14	Sequence 14, Appl
38	26	48.1	7	4	US-09-822-270-9	Sequence 9, Appl
39	26	48.1	9	2	US-08-416-870C-22	Sequence 22, Appl
40	26	48.1	9	2	US-08-340-283-86	Sequence 86, Appl
41	26	48.1	9	3	US-08-895-590-51	Sequence 51, Appl
42	26	48.1	10	1	US-08-230-047-12	Sequence 12, Appl
43	26	48.1	10	3	US-08-476-509B-31	Sequence 31, Appl
44	25	46.3	9	1	US-07-972-032-20	Sequence 20, Appl
45	25	46.3	9	1	US-07-972-032-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-657-163A-2
; Sequence 2, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LIPNS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR EVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULAR TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKMDPTPPL 10
Db 1 LKMDPTPPL 10

RESULT 2
US-09-232-446B-24
Sequence 24, Application US/09232446B

Patent No. 6228647
GENERAL INFORMATION:
APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Transposable Element Protein that Directs DNA
TITLE OF INVENTION: Integration to Specific Chromosomal Sites
FILE REFERENCE: 2-98

CURRENT APPLICATION NUMBER: US/09/232,446B
CURRENT FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 60/071,383
PRIOR FILING DATE: 1998-01-15

NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 6

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
US-09-232-446B-24

Query Match 55.6%; Score 30; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTTP 9
Db 1 LDPSPP 6

RESULT 3
US-09-547-693-168
Sequence 168, Application US/09547693

Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kleiszewski, Marcia

TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 168
LENGTH: 8

TYPE: PRT
ORGANISM: Artificial/Unknown
FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE

LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
LOCATION: (3)..(4)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168

Query Match 55.6%; Score 30; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPL 10
Db 1 PTPPL 5

RESULT 4
US-09-547-693-165
Sequence 165, Application US/09547693

Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kleiszewski, Marcia

TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 165
LENGTH: 10

TYPE: PRT
ORGANISM: Artificial/Unknown
FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE

LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
NAME/KEY: SITE
OTHER INFORMATION: The Proline at this position is a hydroxyproline.

LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-165

Query Match 55.6%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPL 10
Db 3 PTPPL 7

RESULT 5
US-07-989-290-2
Sequence 2, Application US/07989290

Patent No. 5358934
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov

TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL

COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: US/86S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-989-290-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

RESULT 6
US-08-271-698-2
Sequence 2, Application US/08271698
Patent No. 5439821
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: Of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: US/86S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-271-698-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

RESULT 7
US-08-468-596-2
Sequence 2, Application US/08468596
Patent No. 5629196
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: Of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,698
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: US/86S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-596-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

RESULT 8
US-09-295-996B-12

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/ Sequence 12, Application US/09295996B
/ Patent No. 6413530
/ GENERAL INFORMATION:
/ APPLICANT: Borovsky, Dov
/ TITLE OF INVENTION: PESTICIDAL PEPTIDES
/ FILE REFERENCE: UF-230
/ CURRENT APPLICATION NUMBER: US/09/295,996B
/ CURRENT FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 12
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: TMOF peptide
US-09-295-996B-12
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Query Match          50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 5 DPTPP 9
    |||
Db 2 DPAPP 6
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RESULT 9
US-09-295-846B-15
/ Sequence 15, Application US/09295846B
/ Patent No. 6562590
/ GENERAL INFORMATION:
/ APPLICANT: Borovsky, Dov
/ TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
/ FILE REFERENCE: UF-223
/ CURRENT APPLICATION NUMBER: US/09/295,846B
/ CURRENT FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: TMOF peptide
US-09-295-846B-15
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Query Match          50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 5 DPTPP 9
    |||
Db 2 DPAPP 6
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RESULT 10
US-09-551-737C-15
/ Sequence 15, Application US/09551737C
/ Patent No. 6566129
/ GENERAL INFORMATION:
/ APPLICANT: Borovsky, Dov
/ APPLICANT: Schleisinger, Yaakov
/ APPLICANT: Nauwejaers, Sabine M. I.
/ TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
/ FILE REFERENCE: UF-223C1
/ CURRENT APPLICATION NUMBER: US/09/551,737C
/ CURRENT FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 09/295,846
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 15
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/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: TMOF peptide
US-09-551-737C-15
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```
Query Match          50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 5 DPTPP 9
    |||
Db 2 DPAPP 6
```

```
RESULT 11
US-09-295-924B-2
/ Sequence 2, Application US/09295924B
/ Patent No. 6593299
/ GENERAL INFORMATION:
/ APPLICANT: John, Bennett
/ APPLICANT: Alan, Brandt
/ APPLICANT: Dov, Borovski
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
/ FILE REFERENCE: 4137-120
/ CURRENT APPLICATION NUMBER: US/09/295,924B
/ CURRENT FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: ( )
/ OTHER INFORMATION: Truncated TMOF
US-09-295-924B-2
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```
Query Match          50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 5 DPTPP 9
    |||
Db 2 DPAPP 6
```

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RESULT 12
US-09-551-738B-12
/ Sequence 12, Application US/09551738B
/ Patent No. 6635265
/ GENERAL INFORMATION:
/ APPLICANT: Borovsky, Dov
/ TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
/ FILE REFERENCE: UF-224C1
/ CURRENT APPLICATION NUMBER: US/09/551,738B
/ CURRENT FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 09/296,113
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 12
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: TMOF peptide
US-09-551-738B-12
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```
Query Match          50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9

Db 2 DPAP 6

RESULT 13

US-07-989-290-3

Sequence 3, Application US/07989290

Patent No. 5358934

GENERAL INFORMATION:

APPLICANT: Borovsky, Dov

TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290

FILING DATE: 19921211

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UP/S&S-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-375-5800

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

HYPOTHEICAL: NO

ANTI-SENSE: NO

US-07-989-290-3

Query Match 50.0%; Score 27; DB 1; Length 7;

Best Local Similarity 80.0%; Pred. No. 3.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9

Db 2 DPAP 6

RESULT 14

US-08-271-698-3

Sequence 3, Application US/08271698

Patent No. 5439821

GENERAL INFORMATION:

APPLICANT: Borovsky, Dov

TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/271,698

FILING DATE: 07-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290

FILING DATE: 11-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UP/S&S-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

HYPOTHEICAL: NO

ANTI-SENSE: NO

US-08-271-698-3

Query Match 50.0%; Score 27; DB 1; Length 7;

Best Local Similarity 80.0%; Pred. No. 3.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9

Db 2 DPAP 6

RESULT 15

US-08-468-596-3

Sequence 3, Application US/08468596

Patent No. 5629196

GENERAL INFORMATION:

APPLICANT: Borovsky, Dov

TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,596

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/271,698

FILING DATE: 07-JUL-1994

APPLICATION NUMBER: US/07/989,290

FILED DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-596-3

Query Match 50.0%; Score 27; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

Search completed: January 6, 2005, 10:51:58
Job time : 38 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: January 6, 2005, 10:59:50 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-047-945-2

Sequence: 1 LKMDPTPLWKTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28346 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	32.1	7	2	A61081	tryptophyllin, bas
2	27	32.1	10	2	A36454	trypsin-modulating
3	27	32.1	15	2	A47628	Fc gamma receptor
4	25	29.8	13	2	PH1620	Ig H chain V-D-J r
5	25	29.8	15	2	PD0444	coupling factor 6
6	24	28.6	8	2	S21288	lectin - potato (f
7	23	27.4	7	4	A58725	virotaxin - destro
8	23	27.4	12	2	I58273	chryoglobulin - ra
9	23	27.4	15	2	B39109	hypocretin 1.5K
10	23	27.4	15	2	B61457	alpha-glucosidase
11	22	26.2	13	2	G37266	Ig heavy chain C r
12	22	26.2	13	2	D37267	Ig heavy chain C r
13	22	26.2	14	2	PT0026	calotropin DI - mu
14	22	26.2	15	2	PT0037	light harvesting c
15	21	25.0	10	2	C35389	urease (EC 3.5.1.5
16	21	25.0	10	2	B59272	peptide-N4-(N-acet
17	21	25.0	10	2	S39030	lysoyl-bradykinin -
18	21	25.0	11	1	XAV1BH	bradykinin-potent
19	21	25.0	11	2	CS9151	protein-lysine k
20	21	25.0	15	2	PA0055	protein QF20007 -
21	21	25.0	15	2	A26212	carboxypeptidase B
22	20	23.8	5	2	B60274	major protein anti
23	20	23.8	8	2	S10783	enamelin f - bovin
24	20	23.8	8	2	A39308	glycine reductase
25	20	23.8	9	2	S78426	52.5K protein - sp
26	20	23.8	12	1	UTUGO	tremorogen A-10 -
27	20	23.8	12	2	PN0663	dystrophin-associa
28	20	23.8	14	2	PH1348	Ig heavy chain DJ
29	20	23.8	14	2	A60158	disaggregatase - M

30	20	23.8	14	2	S33801	chaperone, TCPI-re
31	20	23.8	14	2	S33802	chaperone, TCPI-re
32	20	23.8	15	2	S10891	ubiquitin thioleat
33	20	23.8	15	2	PT0093	ubiquitin thioleat
34	19	22.6	9	2	B30572	T-cell receptor be
35	19	22.6	9	2	A60108	exocoxin A - Strep
36	19	22.6	9	2	S26508	collagen alpha 2(V
37	19	22.6	10	2	C30572	T-cell receptor be
38	19	22.6	11	2	D45900	complement C3b rec
39	19	22.6	11	2	A45037	TCR gamma V-J regi
40	19	22.6	13	2	A40207	cell surface glyco
41	19	22.6	14	2	F33160	H+-transporting tw
42	19	22.6	14	2	S12904	protein kinase (EC
43	19	22.6	14	2	B56884	Pax-ONR, long form
44	19	22.6	15	2	A60929	dichloromethane de
45	19	22.6	15	2	S67918	serine proteinase

ALIGNMENTS

RESULT 1

A61081
tryptophyllin, basic - Rohde's leaf frog
C/Species: Phyllomedusa rohdei (Rohde's leaf frog)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 18-Aug-2000
C/Accession: A61081
R/MonteCucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
Int. J. Pept. Protein Res. 33, 391-395, 1989
A/Title: Isolation, structure determination and synthesis of a novel tryptophan-contain
A/Reference number: A61081
A/Accession: A61081
A/Molecule type: protein
A/Residues: 1-7 <MON>
C/Comment: The biological activity of this peptide was not determined.
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; hydroxyproline; skin
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
F/7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 32.1%; Score 27; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPMI 12
Db 2 PPSMI 6

RESULT 2

A36454
trypsin-modulating coostatic factor - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #ext_change 09-Jul-2004
C/Accession: A36454; A61630
R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A/Title: Mosquito coostatic factor: a novel decapeptide modulating trypsin-like enzyme b
A/Reference number: A36454; MWID:90367888; PMID:2394318
A/Accession: A36454
A/Molecule type: protein
A/Residues: 1-10 <BOR>
A/Cross-references: UNIPROT:P19425
R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A/Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating coo
A/Reference number: A61630; MWID:93357794; PMID:8353526
A/Accession: A61630
A/Molecule type: protein
A/Residues: 1-10 <BO2>
A/Note: none of the amino acids is modified
C/Function:
A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ei

C/Keywords: hormone

Query Match 32.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
 ||||
 Db 2 DPAP 6

RESULT 3

A47628
Fc gamma receptor II (CD32) - human (fragments)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: A47628

R/Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, B.J.; Capel, P.J.A.

J. Exp. Med. 172, 19-25, 1990

A>Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).

A/Reference number: A47628; MUID:90293679; PMID:2141627

A/Accession: A47628

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-15 <MAR>

C/Keywords: immunoglobulin receptor

Query Match 32.1%; Score 27; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MDPTPLM 11
 ||||
 Db 1 MTAAPPCW 8

RESULT 4

PH1620
Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1620

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1620

A/Molecule type: DNA

A/Residues: 1-13 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 29.8%; Score 25; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TPLPM 11
 ||||
 Db 8 TPLM 12

RESULT 5
 PD0444
 coupling factor 6 mitochondrial - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C/Accession: PD0444

R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: PD0441

A/Contents: Sclatun

A/Accession: PD0444

A/Molecule type: protein
 A/Residues: 1-15 <KAW>
 C/Keywords: mitochondrion

Query Match 29.8%; Score 25; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 5.8e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KAMDPTPLM 12
 ||||
 Db 2 KELDPOKLFV 12

RESULT 6

S21288
lectin - potato (fragment)

C/Species: Solanum tuberosum (potato)

C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: S21288

R/Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Stabae, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A>Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization

A/Reference number: S21288; MUID:92272683; PMID:1590771

A/Accession: S21288

A/Molecule type: protein

A/Residues: 1-8 <MIL>

A/Cross-references: UNIPROT:Q7M1V6

A/Experimental source: var. Ulster Sceptre

A/Function: may be involved in defence mechanism of the plant

C/Keywords: hydroxyproline; lectin

Query Match 28.6%; Score 24; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 7

A58725
virotoxin - destroying angel

C/Species: Amanita virosa (destroying angel)

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C/Accession: A58725

R/Faulstich, H.; Boku, A.; Bodenmuller, H.; Wieland, T.

Biochemistry 19, 334-343, 1980

A>Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.

A/Reference number: A58725; MUID:6893271; PMID:6893271

A/Accession: A58725

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-7 <PAU>

C/Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide

F:1-7/Cross-link: cyclopeptide (Val-Leu) #status experimental

F:2/Modified site: D-threonine (Thr) #status experimental

F:3/Modified site: D-serine (Ser) #status experimental

F:4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental

F:5/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental

F:7/Modified site: 4,5-dihydroxyvaline (Leu) #status experimental

Query Match 27.4%; Score 23; DB 4; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TPLPM 12
 ||||
 Db 2 TSPAM 7

RESULT 8

158273
 thyroglobulin - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_rev1501 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 158273
 R/Mustel, A.M.; Ursell, V.M.; Avvedimento, E.V.; Zimmarino, V.; Di Lauro, R.
 Nucleic Acids Res. 15, 8149-8166, 1987
 A/Title: A cell type specific factor recognizes the rat thyroglobulin promoter.
 A/Reference number: 158273; PMID:8804046; PMID:3671079
 A/Accession: 158273
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-12 <RES>
 A/Cross-references: UNIPROT:Q63579; EMBL:X06162; NID:957368; PIDN:CA29519.1; PID:957368

Query Match 27.4%; Score 23; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.6e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LWKT 14
 |||
 DB 6 LWVST 10

RESULT 9
 B39109
 hypothetical 1.5K protein - hepatitis C virus
 N/Alternate names: hypothetical protein 2
 C/Species: hepatitis C virus
 C/Date: 18-Oct-1991 #sequence_rev1501 18-Oct-1991 #text_change 07-May-1999
 C/Accession: B39109; J01585
 R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urddea, M.S.; Tekamp-
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
 A/Reference number: A39109; PMID:9115678; PMID:1705704
 A/Accession: B39109
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-15 <HAN>
 A/Cross-references: GB:M58406
 R/Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A/Title: Cloning and sequencing of the structural region and expression of putative core
 A/Reference number: J01584; PMID:92300349; PMID:118944
 A/Accession: J01585
 A/Molecule type: genomic RNA
 A/Residues: 1-15 <KUM>
 A/Experimental source: strain U.K.

Query Match 27.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRPPL 10
 |||
 DB 7 PGPPPL 11

RESULT 10
 B61457
 alpha-glucosidase (BC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
 C/Species: Tetrahymena pyriformis
 C/Date: 28-Oct-1994 #sequence_rev1501 28-Oct-1994 #text_change 07-Dec-1999
 C/Accession: B61457
 R/Panno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protoplast. 36, 562-567, 1989
 A/Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
 A/Reference number: A61457; PMID:90055988; PMID:2689637
 A/Accession: B61457
 A/Molecule type: protein
 A/Residues: 1-15 <BAN>
 C/Genetics:
 A/Genetic code: SGCS

C/Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; mono-

Query Match 27.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPPL 10
 |||
 DB 6 TPPL 9

RESULT 11
 G37266
 Ig heavy chain C region (Py2) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 19-Mar-1997 #sequence_rev1501 13-Mar-1998 #text_change 13-Mar-1998
 C/Accession: G37266
 R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A/Reference number: A38740; PMID:91177923; PMID:1706720
 A/Accession: G37266
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-13 <RUF>

Query Match 26.2%; Score 22; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLW 11
 |||
 DB 10 PLW 12

RESULT 12
 D37267
 Ig heavy chain C region (Py69) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 19-Mar-1997 #sequence_rev1501 13-Mar-1998 #text_change 13-Mar-1998
 C/Accession: D37267
 R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
 A/Reference number: A38740; PMID:91177923; PMID:1706720
 A/Accession: D37267
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-13 <RUF>

Query Match 26.2%; Score 22; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLW 11
 |||
 DB 10 PLW 12

RESULT 13
 PT0026
 calotropin DI - mudar (fragment)
 C/Species: Calotropis gigantea (mudar, madar)
 C/Date: 07-Sep-1990 #sequence_rev1501 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: PT0026
 R/Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
 Phytochemistry 26, 633-636, 1987
 A/Title: Chemical modification and amino terminal sequence of calotropin DI from Calotr
 A/Reference number: PT0026
 A/Accession: PT0026
 A/Molecule type: protein
 A/Residues: 1-14 <BHA>
 A/Cross-references: UNIPROT:P20728

C:/Comment: This enzyme is classified as a plant cysteine protease.

C:/Keywords: pyroglutamic acid

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 26.2%; Score 22; DB 2; Length 14;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTPPLW 11

DB 3 PRYPVW 8

RESULT 14

PT0037

Light harvesting complex chain III/b, photosystem I - rice (fragment)

C:/Species: Oryza sativa (rice)

C:/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:/Accession: PT0037; PS0205

R/Uchiyama, Y.; Teugita, A.

submitted to JIPID, June 1991

A:/Reference number: PS0189

A:/Accession: PT0037

A:/Molecule type: protein

A:/Residues: 1-15 <UCH>

A:/Cross-references: UNIPROT:Q7M1V1

Query Match

Best Local Similarity 26.2%; Score 22; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMPTRPP 9

DB 4 EAAAPPP 11

RESULT 15

C35389

urease (BC 3.5.1.5) 6K chain - Morganelle morganii (fragment)

C:/Species: Morganelle morganii

C:/Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004

C:/Accession: C35389

R/Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A:/Title: Morganelle morganii urease: purification, characterization, and isolation of ge

A:/Reference number: A35389; MUID:90264298; PMID:2345135

A:/Accession: C35389

A:/Status: preliminary

A:/Molecule type: protein

A:/Residues: 1-10 <HUA>

A:/Cross-references: UNIPROT:P17339

C:/Keywords: hydrolase

Query Match

Best Local Similarity 25.0%; Score 21; DB 2; Length 10;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9

DB 1 MOUTPP 6

Search completed: January 6, 2005, 11:09:13
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:52:04 ; Search time 188 Seconds
(without alignments)

45,908 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84
Sequence: 1 LKAMPTPLMIKTE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	32.1	7	1	TPFY_PACDA
2	27	32.1	10	1	TMOF_AEDAE
3	27	32.1	14	2	Q9GQP2
4	26	31.0	11	2	Q9UCR1
5	25	29.8	12	2	Q6X7V1
6	25	29.8	12	2	Q8KZ86
7	25	29.8	12	2	AAP79619
8	25	29.8	13	1	ECDE_LYMDI
9	25	29.8	14	2	Q9TEN1
10	25	29.8	14	2	Q9TEN3
11	24	28.6	8	2	Q7MIY6
12	24	28.6	14	2	Q6SRS2
13	24	28.6	14	2	AAR23007
14	23	27.4	10	2	Q76MK5
15	23	27.4	10	2	BAB87160
16	23	27.4	11	2	Q8IVG8
17	23	27.4	11	2	CAA33464
18	23	27.4	12	2	Q63579
19	23	27.4	14	1	TAT_HV1W2
20	23	27.4	14	1	TAT_HV1Z8
21	23	27.4	14	2	Q8HR43
22	23	27.4	14	2	Q8JDM0
23	23	27.4	14	2	Q8JDM3
24	23	27.4	14	2	Q8JDM7
25	23	27.4	14	2	AAL78488
26	22	26.2	11	2	Q8MAZ1
27	22	26.2	11	2	Q8MAZ3
28	22	26.2	11	2	Q8MB39
29	22	26.2	11	2	Q8MB58
30	22	26.2	11	2	Q8MB77
31	22	26.2	11	2	Q8MB79

32	22	26.2	11	2	Q8MB97	Q8mb97 merremia pe
33	22	26.2	11	2	Q8MBE1	Q8mbel ipomoea ald
34	22	26.2	13	2	Q43174	Q43174 solanum tub
35	22	26.2	14	1	CAL1_CALGI	P20728 calotropis
36	22	26.2	15	2	Q9TZG9	Q9tzg9 solanum tub
37	22	26.2	15	2	Q7MIV1	Q7miv1 oryza sativ
38	22	26.2	15	2	Q9S8R4	Q9s8r4 gossypium h
39	21	25.0	6	1	R101_LITRU	P82096 litorea rub
40	21	25.0	9	2	Q9H3Z6	Q9h3z6 homo sapien
41	21	25.0	9	2	Q6SP94	Q6sp94 chlamydomon
42	21	25.0	9	2	Q9J193	Q9j193 pseudomonas
43	21	25.0	9	2	Q9PRJ4	Q9prj4 leplisosteus
44	21	25.0	9	2	AAR20844	Aar20844 chlamydom
45	21	25.0	10	1	BRK_ONCMY	Q9prz1 oncorhynch

ALIGNMENTS

RESULT 1	ID	TPFY_PACDA	STANDARD;	PRT;	7 AA.
AC P83455;					
DT 28-FEB-2003 (Rel. 41, Last Created)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Tryptophyllin-1 (Pdt-1)					
OS Pachymedusa daemicolor (Giant Mexican leaf frog)					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;					
OC Phyllomedusinae; Pachymedusa.					
NCBI_Taxid=75988;					
RN [1]					
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.					
RA TISSUE-Skin secretion;					
RC Chen T.B., Orr D.F., Shaw C.;					
RT "Pachymedusa daemicolor tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA."					
RL Submitted (SBP-2002) to Swiss-Prot.					
CC -1- FUNCTION: Myosin-like. Has selective relaxing activity on vascular smooth muscle.					
CC -1- SUBCELLULAR LOCATION: Secreted.					
CC -1- TISSUE SPECIFICITY: Skin.					
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.					
DR GO: GO:000576; C:extracellular; NAS.					
DR GO: GO:0045986; P:negative regulation of smooth muscle contractility; NAS.					
KW Amidation; Amphibian defense peptide; Direct protein sequencing;					
KW Hydroxylation.					
FT MOD RES 3					
FT MOD RES 7					
FT MOD RES 7					
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;					
Query Match					
Best Local Similarity					
Matches					
3; Conservative					
1; Mismatches					
1; Indels					
Gaps					
0;					
RESULT 2					
TMOF_AEDAE					
ID TMOF_AEDAE					
AC P19435;					
DT 01-NOV-1990 (Rel. 16, Last Created)					
DT 01-NOV-1990 (Rel. 16, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Tryptsin-modulating coelastatin factor (TMOF) (OOSH).					
OS Aedes aegypti (Yellowfever mosquito).					
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OX NCBI_TaxID=7159;

RP STRAIN=Vero beach; TISSUE=Ovary;
 RC MEDLINE=90367886; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
 enzyme biosynthesis in the midgut.";
 RL PNASB J. 4:3015-3020 (1990).
 RN [2]

RP STRAIN=Vero beach; TISSUE=Ovary;
 RC MEDLINE=93357794; PubMed=8353526;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 modulating oostatic factor (TMOF) and its analogs.";
 RL Insect Biochem. Mol. Biol. 23:703-712 (1993).
 CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 in the midgut which indirectly reduces the vitellogenin
 concentration in the hemolymph resulting in inhibition of oocyte
 development.

CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
 and stops at 56 hrs.
 CC PIR: A36454; A36454.
 KW Direct protein sequencing; Hormone.

FT VARIANT 3 10 Poly-Pro.
 FT YD->DY (TN TMFO(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 32.1%; Score 27; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
 DB 2 DPAAP 6

RESULT 3
 Q96QP2 PRELIMINARY; PRT; 14 AA.

AC Q96QP2; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tissue factor pathway inhibitor-2 (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RA MEDLINE=22643823; PubMed=12757776;
 RA Hude F., Reverdiu P., Iochmann S., Cherpi-Antar C., Gruel Y.;
 RT "Characterization and functional analysis of TPPI-2 gene promoter in a
 human choriocarcinoma cell line.";
 RL Thromb. Res. 109:207-215 (2003).
 DR EMBL; AY044097; AKK72693.1; -.

FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1509 MW; 4E70ED6001BC1177 CRC64;

Query Match 32.1%; Score 27; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPL 10
 DB 1 MDPAAPL 7

RESULT 4

G9UCR1 PRELIMINARY; PRT; 11 AA.

AC G9UCR1; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE AUTOTAXIN (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE.
 RX MEDLINE=92129337; PubMed=1733949;
 RA Stracke M.L., Knuttsch H.C., Unsworth E.J., Arestad A., Cloce V.,
 RA Schiffmann E., Liotta L.A.;
 RT "Identification, purification, and partial sequence analysis of
 autotaxin, a novel motility-stimulating protein.";
 RL J. Biol. Chem. 267:2524-2529 (1992).

FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 31.0%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLMT 12
 DB 4 PLMT 7

RESULT 5
 Q6X7V1 PRELIMINARY; PRT; 12 AA.

AC Q6X7V1; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Insulin-like factor 3 (Fragment).

GN Name=INSI3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22929740; PubMed=12890727;
 RA Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulunk A.I.;
 RT "Isolation and expression analysis of the canine insulin-like factor 3
 gene.";
 RL Biol. Reprod. 69:1658-1664 (2003).

DR EMBL; AY251015; AAP79619.1; -.

FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1354 MW; 20BD91ADFA7DD737 CRC64;

Query Match 29.8%; Score 25; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPTPLM 11
 DB 1 MSPRPLAW 8

RESULT 6
 Q8KZ86 PRELIMINARY; PRT; 12 AA.

AC Q8KZ86; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Class I integrin DNA integrase (Fragment).


```

GN Name=inf1;
OS Acinetobacter baumannii.
OC Bacteri; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22270987; PubMed=12384388;
RA Gomboc F., Ricci M.L., Roscolini G.M., Lagatolla C., Tonin E.,
RA Monti-Bragadin C., Lavenia A., Dolzani L.;
RT "Molecular characterization of integrins in epidemiologically
RT unrelated clinical isolates of Acinetobacter baumannii from Italian
RT hospitals reveals a limited diversity of gene cassette arrays.";
RL Antimicrob. Agents Chemother. 46:3665-3668(2002).
DR EMBL; AJ31334; CAC85941.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1296 MW; 9042688F5E376DC1 CRC64;

Query Match 29.8%; Score 25; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3.6e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 4 ATAPLPPL 11

RESULT 7
ID AAP79619 PRELIMINARY; PRT; 12 AA.
AC AAP79619;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Insulin-like factor 3 (Fragment).
OS INSL3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12890727;
RA Tuong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.;
RT "Isolation and Expression Analysis of the Canine Insulin-Like Factor 3
RT Gene.";
RL Biol. Reprod. 69:1658-1664(2003).
DR EMBL; AY251015; AAP79619.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;

Query Match 29.8%; Score 25; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPPTPLM 11
DB 1 MSPRPLAW 8

RESULT 8
ID ECDE_LYMDI STANDARD; PRT; 13 AA.
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Testis ecdysiotropin peptide B (TEB).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;

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RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of
CC larvae and pupae.
KM Direct protein sequencing.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 29.8%; Score 25; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
DB 2 AIDPNP 7

RESULT 9
ID OPTEN1 PRELIMINARY; PRT; 14 AA.
AC OPTEN1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE ATPase 8 (Fragment).
OS Anas castanea (Chestnut teal).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=45631;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennedy M., Spencer H.G.;
RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
RL Auk 117:154-163(2000).
DR EMBL; AF173494; AAD51052.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER 1
SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;

Query Match 29.8%; Score 25; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTPPLM 11
DB 6 PTPPMW 11

RESULT 10
ID OPTEN3 PRELIMINARY; PRT; 14 AA.
AC OPTEN3;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE ATPase 8 (Fragment).
OS Anas gracilis (Grey teal).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=45630;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennedy M., Spencer H.G.;
RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";

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RL Auk 117:154-163(2000).
 DR EMBL; AF173493; AAD51050.1; -.
 GO GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER 1

SEQUENCE 14 AA; 1672 MW; 80FB803727P9B871 CRC64;

Query Match 29.8%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 PTPPLW 11
 DB 6 PTPPWW 11

RESULT 11

O7M1V6 PRELIMINARY; PRT; 8 AA.

AC O7M1V6; (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Lectin (Fragment).

OS Solanum tuberosum (potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Solanales; Solanaceae; Solanum.

NCBI_Taxid=4113;

FT NON_TER 1

FT NON_TER 8

FT NON_TER 1

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Query Match 28.6%; Score 24; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 PTPPL 10
 DB 4 PLPPL 8

RESULT 13

AAR23007 PRELIMINARY; PRT; 14 AA.

AC AAR23007; (TREMBLrel. 27, Created)

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)

DE Pgl (Fragment).

OS Drosophila simulans (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_Taxid=7240;

FT NON_TER 1

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SEQUENCE 14 AA; 1456 MW; 2C83E49CCDBE7E37 CRC64;

Query Match 28.6%; Score 24; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 PTPPL 10
 DB 4 PLPPL 8

RESULT 14

O76MK5 PRELIMINARY; PRT; 10 AA.

AC O76MK5; (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE ATPase subunit 8 (Fragment).

OS Eurypharynx pelecanoides (pelican eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;

OC Eurypharyngidae; Eurypharynx.

NCBI_Taxid=55117;

FT NON_TER 1

FT NON_TER 1

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SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
 :||:|
 Db 4 LDBSP 8

RESULT 15

BAB87160 PRELIMINARY; PRT; 10 AA.
 AC BAB87160;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATPase 8.
 OS Eurypharynx pelecanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Bel.",
 RL Mol. Biol. Evol. 20:1917-1924 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046487; BAB87160.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
 :||:|
 Db 4 LDBSP 8

Search completed: January 6, 2005, 11:08:29
 Job time : 190 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:51:24 ; Search time 149 Seconds
(without alignments)
36.114 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPPLPWIKTB 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	AAW1575	AAW1575 N-terminu
2	84	100.0	15	AAW53841	AAW53841 N-terminu
3	84	100.0	15	ABB80223	ABB80223 Synthetic
4	69	82.1	12	ABB80225	ABB80225 Synthetic
5	65	77.4	11	ABB80226	ABB80226 Synthetic
6	54	64.3	10	AAW53843	AAW53843 N-terminu
7	54	64.3	10	ABB80222	ABB80222 Synthetic
8	50	59.5	9	ABB80227	ABB80227 Synthetic
9	43	51.2	8	ABB80228	ABB80228 Synthetic
10	41	48.8	9	ABR12621	ABR12621 Human can
11	41	48.8	9	ABR12621	ABR12621 Human can
12	41	48.8	9	ABR12854	ABR12854 Human can
13	41	48.8	10	ABR12743	ABR12743 Human can
14	41	48.8	10	ABR11875	ABR11875 Human can
15	41	48.8	10	ABR12121	ABR12121 Human can
16	41	48.8	10	ABR12948	ABR12948 Human can
17	41	48.8	10	ABR12106	ABR12106 Human can
18	41	48.8	10	ABR12294	ABR12294 Human can
19	41	48.8	10	ABR12738	ABR12738 Human can
20	41	48.8	15	ABR33125	ABR33125 Human can
21	41	48.8	15	ABR33383	ABR33383 Human can
22	41	48.8	15	ABR33116	ABR33116 Human can
23	41	48.8	15	ABR33427	ABR33427 Human can
24	41	48.8	15	ABR33363	ABR33363 Human can
25	38	45.2	9	AAW21252	AAW21252 Hydroxyme

26	37	44.0	9	ABR11778	ABR11778 Human can
27	37	44.0	9	ABR12206	ABR12206 Human can
28	37	44.0	10	ABR12924	ABR12924 Human can
29	37	44.0	10	AD064358	AD064358 Human 213
30	37	44.0	15	AAW39043	AAW39043 Peptide r
31	37	44.0	15	ABR33382	ABR33382 Human can
32	36	42.9	9	ABR12770	ABR12770 Human can
33	36	42.9	9	ABR12969	ABR12969 Human can
34	36	42.9	9	ABR12458	ABR12458 Human can
35	36	42.9	9	ABR12601	ABR12601 Human can
36	36	42.9	9	ABR12046	ABR12046 Human can
37	36	42.9	9	ABR12234	ABR12234 Human can
38	36	42.9	9	AD072393	AD072393 Human 213
39	36	42.9	9	AD072483	AD072483 Human 213
40	36	42.9	9	AD072536	AD072536 Human 213
41	36	42.9	9	AD072664	AD072664 Human 213
42	36	42.9	9	AD072353	AD072353 Human 213
43	36	42.9	9	AD072482	AD072482 Human 213
44	36	42.9	9	AD064670	AD064670 Human 213
45	36	42.9	8	AD065216	AD065216 Human 213

ALIGNMENTS

RESULT 1	AAW1575	standard; peptide; 15 AA.
XX	AAW1575;	
AC	XX	
DT	25-MAR-2003 (revised)	
DT	20-MAR-1997 (first entry)	
DE	XX	
DE	N-terminal peptide from lethal toxin neutralising factor.	
KW	lethal toxin neutralising factor; LTNF; opoosum; bee toxin;	
KW	scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.	
XX	XX	
OS	Didelphis virginiana.	
XX	XX	
PN	US576297-A.	
XX	XX	
PD	19-NOV-1996.	
XX	XX	
PF	22-SBP-1994; 94US-00310340.	
XX	XX	
PR	10-MAY-1993; 93US-00058387.	
PA	(LIPF/) LIPPS B V.	
PA	(LIPF/) LIPPS F W.	
PI	Lipps FW, Lipps BV;	
DR	WPI; 1997-011287/01.	
XX	XX	
PT	Treatment of victims of bee or scorpion stings or plant or bacterial	
PT	toxins - by admin. of lethal toxin-neutralising factor or its N-terminal	
PT	peptide.	
XX	XX	
PS	Claim 7; Col 9; 9pp; English.	
CC	XX	
CC	The present sequence is from the N-terminus of a 68 kD protein purified	
CC	from the serum of the opossum Didelphis virginiana. The full-length	
CC	protein is a lethal toxin neutralising factor (LTNF). The use of purified	
CC	LTNF or of the chemically synthesised 15mer N-terminal peptide for	
CC	treating victims of bee stings, scorpion stings and bacterial or plant	
CC	toxins is claimed. The patent disclosure does not provide any evidence	
CC	for neutralising activity against these various toxins. There is evidence	
CC	of significant neutralising activity of the opossum LTNF and the 15mer	
CC	peptide against venom from snakes of the families Crotalidae, Elapidae,	
CC	Hydroiidae and Viperaidae. (Updated on 25-MAR-2003 to correct PF field.)	
XX	XX	

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
1 LKAMDPTPLMIKTE 15

RESULT 2

AAM53841 AAM53841 standard; peptide; 15 AA.

XX AAM53841;

AC AAM53841;

DT 08-JUL-1998 (first entry)

DE N-terminus of opossum LTNP.

XX LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;

KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;

KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;

XX histamine reaction treatment.

XX Didelphis virginiana.

PN US5744449-A.

PD 28-APR-1998.

PF 03-JUN-1996; 96US-00657163.

PR 10-MAY-1993; 93US-00058387.

PR 22-SEP-1994; 94US-00310340.

PA (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.

PI LIPPS FW, LIPPS BV;

DR WPI; 1998-271108/24.

PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

XX Claim 1; Col 11; 11pp; English.

This sequence represents the peptide of the invention. It is a lethal toxin neutralising factor (LTNP) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity to horse proteins

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
1 LKAMDPTPLMIKTE 15

RESULT 3

ABB80223 ABB80223 standard; peptide; 15 AA.

XX ABB80223;

AC ABB80223;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNP, LT-15.

XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;

KW IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;

KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;

KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;

KW Graves' disease; Addison's disease; Hodgkin's disease; depression;

KW saliva; ELISA.

XX Synthetic.

OS WO2003060471-A2.

PN 24-JUL-2003.

PD 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.

PI LIPPS BV, LIPPS FW;

DR WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

XX Claim 3; Page 3; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGF levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
1 LKAMDPTPLMIKTE 15

RESULT 4

ABB80225

```

ID ABB80225 standard; peptide; 12 AA.
XX
AC ABB80225;
XX
DT 06-NOV-2003 (first entry)
XX
DE Synthetic LTNF, LT-12.
XX
KM Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
KM saliva; ELISA.
XX
OS Synthetic.
XX
PN WO2003060471-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
PR 14-JAN-2002; 2002US-00047945.
XX
PA (LIPP/) LIPPS B V.
XX (LIPP/) LIPPS F W.
XX
PI Lippe BV, Lipps FW;
XX
DR WPI; 2003-636703/60.
XX
PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
PS Claim 7; Page 4; 24pp; English.
XX
CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA
XX
SQ Sequence 12 AA;
XX
Query Match 82.1%; Score 69; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLMI 12
Db 1 LKAMDPTPLMI 12

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```

XX
DT 06-NOV-2003 (first entry)
XX
DE Synthetic LTNF, LT-11.
XX
KM Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
KM saliva; ELISA.
XX
OS Synthetic.
XX
PN WO2003060471-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
PR 14-JAN-2002; 2002US-00047945.
XX
PA (LIPP/) LIPPS B V.
XX (LIPP/) LIPPS F W.
XX
PI Lippe BV, Lipps FW;
XX
DR WPI; 2003-636703/60.
XX
PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
PS Claim 7; Page 4; 24pp; English.
XX
CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA
XX
SQ Sequence 11 AA;
XX
Query Match 77.4%; Score 65; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLM 11
Db 1 LKAMDPTPLM 11

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RESULT 5
ABB80226
ID ABB80226 standard; peptide; 11 AA.
XX
AC ABB80226;
XX

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```

RESULT 6
AAW53843
ID AAW53843 standard; peptide; 10 AA.
XX
AC AAW53843;
XX
DT 08-JUL-1998 (first entry)
XX

```

DE N-terminus of opossum LTNF.
 XX LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 XX anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KM sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 XX histamine reaction treatment.
 OS Didelphis virginiana.
 PM US5744449-A.
 PM 28-APR-1998.
 PD 03-JUN-1996; 96US-00657163.
 PF 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX LIPPS FW, LIPPS BV;
 PI WPI; 1998-271108/24.
 DR Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 PT
 XX
 XX
 PS Claim 7, col 11; lpp: English.
 CC This sequence represents the peptide of the invention. It is a lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 CC
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 64.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 LKAMPPTPL 10
 |||||
 Db 1 LKAMPPTPL 10
 RESULT 7
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 AC ABB80222;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-10.
 XX
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B;
 KM IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; achute; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.
 XX
 XX Synthetic.

XX	WO2003060471-A2.
PM	
XX	
PD	24-JUL-2003.
XX	
PF	14-JAN-2003; 2003WO-US001044.
XX	
PR	14-JAN-2002; 2002US-00047945.
XX	
PA	(LIPF/) LIPPS B V.
XX	(LIPF/) LIPPS F W.
PI	Lipps BV, Lipps FW;
XX	
DR	WPI, 2003-636703/60.
XX	
PT	Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT	Inulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT	asthma or diabetes, by employing an ELISA on a saliva sample from a
PT	patient.
XX	
PS	Claim 7; Page 3; 24pp; English.
XX	
CC	The sequences given in ABB80222-28 represent lethal toxin neutralising
CC	factor (LTNF) peptides which may be used for reducing elevated levels of
CC	serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC	(NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC	particular, the methods of the invention are useful for diagnosing and
CC	treating conditions with elevated serum IgE levels, e.g. asthma,
CC	diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
CC	arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC	Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC	the protein may be monitored by assaying a human endogenous protein by
CC	performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC	sample using an anti-serum that is specific for the protein. Saliva
CC	collection is relatively non-invasive when compared to blood collection
CC	for serum. Saliva can be centrifuged immediately, whereas blood requires
CC	clotting time before centrifugation to separate serum. Saliva proteins
CC	can be assayed by a simple ELISA test, whereas an assay of proteins from
CC	serum requires a more complicated sandwich type ELISA
XX	
SQ	Sequence 10 AA;
XX	
Query Match	64.3%; Score 54; DB 7; Length 10;
Best Local Similarity	100.0%; Pred. No. 0.074;
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 LKAMPPTPL 10
Dd	1 LKAMPPTPL 10
RESULT 8	
ABBS0227	
ID	ABBS0227 standard; peptide; 9 AA.
AC	ABBS0227;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Synthetic LTNF, LT-9.
XX	
KM	Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KM	IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KM	ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KM	SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KM	Graves' disease; Addison's disease; Hodgkin's disease; depression;
KM	saliva; ELISA.
XX	
OS	Synthetic.
XX	
PN	WO2003060471-A2.
XX	


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PD 24-JUL-2003.
XX
XX 14-JAN-2003; 2003WO-US001044.
XX
XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPF/) LIPPS B V.
XX (LIPF/) LIPPS F W.
XX
XX LIPPS BV, LIPPS FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNP) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
XX Sequence 9 AA;
XX
XX Query Match 59.5%; Score 50; DB 7; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LKAMDPTTP 9
XX |||||
XX 1 LKAMDPTTP 9
XX
XX Db
XX
XX RESULT 9
XX ABB80228
XX ID ABB80228 standard; peptide; 8 AA.
XX
XX AC ABB80228;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE Synthetic LTNP, LT-8.
XX
XX XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
XX KM IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
XX KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematous;
XX KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
XX KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
XX KM saliva; ELISA.
XX
XX OS Synthetic.
XX
XX XX WO2003060471-A2.
XX
XX PD 24-JUL-2003.
XX
XX 14-JAN-2003; 2003WO-US001044.

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XX
XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPF/) LIPPS B V.
XX (LIPF/) LIPPS F W.
XX
XX LIPPS BV, LIPPS FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNP) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
XX Sequence 8 AA;
XX
XX Query Match 51.2%; Score 43; DB 7; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LKAMDPTP 8
XX |||||
XX 1 LKAMDPTP 8
XX
XX Db
XX
XX RESULT 10
XX ABR12621
XX ID ABR12621 standard; peptide; 9 AA.
XX
XX AC ABR12621;
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 156P1D4 HLA peptide #856.
XX
XX KM Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KM human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX XX WO200283921-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 10-APR-2002; 2002WO-US011654.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX

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PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 PS Claim 13; Page 238; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SQ Sequence 9 AA;
 Query Match 48.8%; Score 41; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 MDPPTPLMT 12
 |||:|:|
 1 MDPSPVPIWI 9
 Db
 RESULT 11
 ABR12017
 ID ABR12017 standard; peptide; 9 AA.
 XX
 AC ABR12017;
 DT 19-MAY-2003 (first entry)
 XX
 DB Human cancer-related protein 156PID4 HLA peptide #252.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX

PS Claim 13; Page 232; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SQ Sequence 9 AA;
 Query Match 48.8%; Score 41; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 MDPPTPLMT 12
 |||:|:|
 1 MDPSPVPIWI 9
 Db
 RESULT 12
 ABR12854
 ID ABR12854 standard; peptide; 9 AA.
 XX
 AC ABR12854;
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 156PID4 HLA peptide #1089.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 240; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;

QY Query Match 48.8%; Score 41; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 4 MDPPTPLMI 12
1 MDPSVPIWI 9

RESULT 13
ABR12743
ID ABR12743 standard; peptide; 10 AA.
AC ABR12743;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P14 HLA peptide #978.

XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.

XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.

XX Jakobovits A, Chailita-Bid PM, Farris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.

XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX

PS Claim 13; Page 239; 1021pp; English.

XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX

SQ Sequence 10 AA;

Query Match 48.8%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLMI 12
Db 1 MDPSVPIWI 9

RESULT 14
ABR1875
ID ABR1875 standard; peptide; 10 AA.
AC ABR1875;
XX

DT 19-MAY-2003 (first entry)
XX

DE Human cancer-related protein 156P14 HLA peptide #110.

XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
OS Homo sapiens.

XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011654.

XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Chailita-Bid PM, Farris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.

XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX

PS Claim 13; Page 231; 1021pp; English.

XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX

SQ Sequence 10 AA;

QY Query Match 48.8%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 MDPPTPLMI 12
2 MDPSVPIWI 10

RESULT 15
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ID ABR12121 standard; peptide; 10 AA.

AC ABR12121;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 156P1D4 HLA peptide #356.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KM human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 233; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 10 AA;
 Query Match 48.8%; Score 41; DB 6; Length 10;
 Best local Similarity 66.7%; Pred. No. 8.5;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 MDPPTPLMI 12
 |||:|:|
 Db 1 MDPSPVPIWI 9

Search completed: January 6, 2005, 11:05:15
 Job time : 151 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 11:08:35 ; Search time 141 Seconds
(without alignments)
38.359 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84
Sequence: 1 LKAMDPTPLMKTRE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 251122

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	US-10-047-945-2	Sequence 2, App1
2	69	82.1	12	US-10-047-945-4	Sequence 4, App1
3	65	77.4	11	US-10-047-945-5	Sequence 5, App1
4	54	64.3	10	US-10-047-945-1	Sequence 1, App1
5	50	59.5	9	US-10-047-945-6	Sequence 6, App1
6	43	51.2	8	US-10-047-945-7	Sequence 7, App1
7	37	44.0	15	US-10-161-791-444	Sequence 444, App
8	34	40.5	12	US-10-286-457-239	Sequence 239, App
9	34	40.5	12	US-10-327-598-735	Sequence 735, App
10	33	39.3	9	US-10-057-475B-10923	Sequence 10923, A
11	33	39.3	9	US-10-154-884B-10923	Sequence 10923, A
12	33	39.3	13	US-10-468-370-501	Sequence 501, App
13	33	39.3	13	US-10-468-370-502	Sequence 502, App

14	33	39.3	13	US-10-468-496-457	Sequence 457, App
15	33	39.3	13	US-10-468-496-458	Sequence 458, App
16	32	38.1	12	US-10-185-815-6	Sequence 6, App1
17	32	38.1	12	US-10-161-791-252	Sequence 252, App1
18	32	38.1	12	US-10-116-275-52	Sequence 52, App1
19	32	38.1	13	US-09-966-782A-27	Sequence 27, App1
20	32	38.1	13	US-10-254-905-27	Sequence 27, App1
21	32	38.1	14	US-09-845-583-13	Sequence 13, App1
22	32	38.1	14	US-10-162-497-70	Sequence 70, App1
23	32	38.1	14	US-10-437-708-160	Sequence 160, App
24	32	38.1	14	US-10-257-199-160	Sequence 160, App
25	31	36.9	13	US-10-611-440-188	Sequence 188, App
26	31	36.9	13	US-10-437-708-24	Sequence 24, App1
27	31	36.9	13	US-10-437-708-198	Sequence 198, App
28	31	36.9	13	US-10-395-402-24	Sequence 24, App1
29	31	36.9	13	US-10-257-199-24	Sequence 24, App1
30	31	36.9	13	US-10-257-199-198	Sequence 198, App
31	31	36.9	14	US-09-932-613-192	Sequence 192, App
32	31	36.9	14	US-09-932-613-225	Sequence 225, App
33	31	36.9	14	US-09-932-322-192	Sequence 192, App
34	31	36.9	14	US-09-932-322-225	Sequence 225, App
35	31	36.9	15	US-10-282-960-53	Sequence 53, App1
36	30	35.7	8	US-10-437-708-168	Sequence 168, App
37	30	35.7	8	US-10-257-199-168	Sequence 168, App
38	30	35.7	10	US-10-190-082-480	Sequence 480, App
39	30	35.7	10	US-10-437-708-165	Sequence 165, App
40	30	35.7	10	US-10-257-199-165	Sequence 165, App
41	30	35.7	12	US-09-995-804A-4	Sequence 4, App1
42	30	35.7	12	US-10-225-567A-2288	Sequence 2288, App
43	30	35.7	13	US-10-437-708-21	Sequence 21, App1
44	30	35.7	13	US-10-437-708-22	Sequence 22, App1
45	30	35.7	13	US-10-437-708-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-10-047-945-2
Sequence 2, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BIRNIE V.
TITLE OF INVENTION: DIAGNOSTIC AND TREATMENT FOR IMMUNOGLOBULIN E
FILE REFERENCE: FWLPAT015US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY:
LOCATION:
OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM CROSSM
US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 LKAMDPTPLMKTRE 15
1 LKAMDPTPLMKTRE 15

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US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US2003015755SA1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4
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Query Match      82.1%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LKAMPPTPLWI 12
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DB      1 LKAMPPTPLWI 12
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RESULT 3
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US2003015755SA1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5
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        |||||
DB      1 LKAMPPTPLWI 11
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US-10-047-945-1
; Sequence 1, Application US/10047945
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; Publication No. US2003015755SA1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM CROSSUM
US-10-047-945-1
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Query Match      64.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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        |||||
DB      1 LKAMPPTPL 10
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; Sequence 6, Application US/10047945
; Publication No. US2003015755SA1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LKAMPPTPL 9
        |||||
DB      1 LKAMPPTPL 9
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RESULT 6
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US2003015755SA1
; GENERAL INFORMATION:
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```

; APPLICANT: LIPPS, BIRNIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 7
US-10-161-791-444
; Sequence 444, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLEN, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLER, Dana M.
; APPLICANT: RIDER, James B.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mastrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 444:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-444

Query Match
Best Local Similarity 44.0%; Score 37; DB 14; Length 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 5 RALDPTPL 13

RESULT 8
US-10-286-457-239
; Sequence 239, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPC-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 239
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-239

Query Match
Best Local Similarity 40.5%; Score 34; DB 14; Length 12;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPTWLTQ 15
DB 3 PPTWLTQ 10

RESULT 9
US-10-327-598-735
; Sequence 735, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Hongliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 735
; LENGTH: 12
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-735

Query Match
Best Local Similarity 40.5%; Score 34; DB 16; Length 12;

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Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KANDPTTP 9
Db 1 QSPDPTTP 8

RESULT 10

US-10-057-4758-10923
; Sequence 10923, Application US/100574758
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,4758
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10923
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-057-4758-10923

Query Match 39.3%; Score 33; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLMIKT 14
Db 3 PPLMRT 9

RESULT 11

US-10-154-884B-10923
; Sequence 10923, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10923
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-154-884B-10923

Query Match 39.3%; Score 33; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLMIKT 14
Db 3 PPLMRT 9

RESULT 12

US-10-468-370-501
; Sequence 501, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05


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; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 501
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-501

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Query Match      39.3%; Score 33; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      7 TPTPLWTKT 14
         |||:|
Db      4 TSPTWLKT 11

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RESULT 13
US-10-468-370-502
; Sequence 502, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-502

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```

Query Match      39.3%; Score 33; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      7 TPTPLWTKT 14
         |||:|
Db      1 TSPTWLKT 8

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RESULT 14
US-10-468-496-457
; Sequence 457, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham

```

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; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 2036
; SEQ ID NO 457
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-457

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```

Query Match      39.3%; Score 33; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

QY      7 TPTPLWTKT 14
         |||:|
Db      4 TSPTWLKT 11

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RESULT 15
US-10-468-496-458
; Sequence 458, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458
; LENGTH: 13
; TYPE: PRT

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; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: MHC class II binding epitope
 US-10-468-496-458

Query Match 39.3%; Score 33; DB 16; Length 13;
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 7 TPPLWIKT 14
 Db 1 TSPTWIKT 8

Search completed: January 6, 2005, 11:20:33
 Job time : 142 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 11:02:50 ; Search time 37 Seconds

(without alignments)
26.886 Million cell updates/sec

Title: US-10-047-945-2

Sequence: 1 LKAMPPTPLMKTB 15

Scoring table: BLOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0
Maximum DB seq length: 15Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/aa/PTUS.COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	1	US-08-310-340A-1
2	84	100.0	15	1	US-08-657-163A-1
3	54	64.3	10	1	US-08-657-163A-2
4	37	44.0	15	3	US-08-602-999A-444
5	37	44.0	15	4	US-09-500-124-444
6	32	38.1	11	1	US-08-336-343A-31
7	32	38.1	11	3	US-08-652-877-31
8	32	38.1	11	3	US-08-476-515A-31
9	32	38.1	12	3	US-08-602-999A-252
10	32	38.1	12	4	US-09-500-124-252
11	32	38.1	14	3	US-09-268-992-70
12	32	38.1	14	3	US-09-657-474-70
13	32	38.1	14	4	US-09-845-583A-13
14	32	38.1	14	4	US-09-547-693-160
15	31	36.9	13	3	US-09-232-446B-11
16	31	36.9	13	4	US-09-119-507B-24
17	31	36.9	13	4	US-08-897-556A-24
18	31	36.9	13	4	US-09-547-693-24
19	31	36.9	13	4	US-09-547-693-198
20	30	35.7	6	3	US-09-232-446B-24
21	30	35.7	8	4	US-09-547-693-168
22	30	35.7	10	4	US-09-547-693-165
23	30	35.7	12	2	US-08-659-984A-8
24	30	35.7	12	3	US-08-660-531-8
25	30	35.7	12	4	US-09-995-804B-4
26	30	35.7	13	4	US-09-119-507B-21
27	30	35.7	13	4	US-09-119-507B-22

28	30	35.7	13	4	US-09-119-507B-23	Sequence 23, Appl
29	30	35.7	13	4	US-08-897-556A-21	Sequence 21, Appl
30	30	35.7	13	4	US-08-897-556A-22	Sequence 22, Appl
31	30	35.7	13	4	US-08-897-556A-23	Sequence 23, Appl
32	30	35.7	13	4	US-09-547-693-21	Sequence 21, Appl
33	30	35.7	13	4	US-09-547-693-22	Sequence 22, Appl
34	30	35.7	13	4	US-09-547-693-23	Sequence 23, Appl
35	30	35.7	13	4	US-09-547-693-195	Sequence 195, App
36	30	35.7	13	4	US-09-547-693-197	Sequence 197, App
37	30	35.7	14	2	US-08-687-956A-4	Sequence 4, Appl
38	30	35.7	14	2	US-08-659-984A-11	Sequence 11, Appl
39	30	35.7	14	3	US-08-660-531-11	Sequence 11, Appl
40	30	35.7	14	4	US-09-547-693-196	Sequence 196, App
41	30	35.7	15	4	US-09-148-712-24	Sequence 24, Appl
42	29	34.5	12	4	US-09-315-926A-18	Sequence 18, Appl
43	29	34.5	15	1	US-08-185-432-11	Sequence 11, Appl
44	29	34.5	15	3	US-08-602-999A-385	Sequence 385, App
45	29	34.5	15	3	US-08-602-999A-452	Sequence 452, App

ALIGNMENTS

RESULT 1
US-08-310-340A-1
Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD

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/ INDIVIDUAL ISOLATE: TEXAS WILD
/ DEVELOPMENTAL STAGE: ADULT
/ HAPLOTYPE:
/ TISSUE TYPE: BLOOD
/ CELL TYPE:
/ ORGANELLE:
/ IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
/ LIBRARY:
/ CLONE:
/ PUBLICATION INFORMATION:
/ AUTHORS: JONAS PERALES, ET AL.
/ TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
/ JOURNAL: INTERNATIONAL SOCIETY ON
/ JOURNAL: TOXINOLOGY
/ VOLUME: 10TH WORLD CONGRESS ON ANIMAL
/ VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
/ ISSUE: SINGAPORE
/ PAGES: 104
/ DATE: 3-8 NOV 1991
/
US-08-310-340A-1
/
Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKANDPTPLMIKTE 15
DB 1 LKANDPTPLMIKTE 15

RESULT 2
US-08-657-163A-1
/ Sequence 1, Application US/08657163A
/ Patent No. 574449
/ GENERAL INFORMATION:
/ APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
/ TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
/ TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR
/ TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BINIE V. LIPPS
/ STREET: 4509 MIMOSA DR.
/ CITY: BELLAIRE
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77401
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
/ COMPUTER: IBM COMPATIBLE
/ OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
/ SOFTWARE: MS WORD 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/657,163A
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/310,340
/ FILING DATE: 22 SEPTEMBER 1994
/ CLASSIFICATION: 514
/ APPLICATION NUMBER: 08/058,387
/ FILING DATE: 10 MAY 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: JOHN R. CASPERSON
/ REGISTRATION NUMBER: 28,198
/ REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713-482-2961
/ TELEFAX: 713-663-7290
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 1:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: AMINO ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
/ MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N
/ ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
/ ORGANISM: DIDELPHIS VIRGINIANA
/ STRAIN: WILD
/ INDIVIDUAL ISOLATE: TEXAS WILD
/ DEVELOPMENTAL STAGE: ADULT
/ HAPLOTYPE:
/ TISSUE TYPE: BLOOD
/ CELL TYPE:
/ ORGANELLE:
/ IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
/ LIBRARY:
/ CLONE:
/ PUBLICATION INFORMATION:
/ AUTHORS: JONAS PERALES, ET AL.
/ TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
/ JOURNAL: INTERNATIONAL SOCIETY ON
/ JOURNAL: TOXICOLOGY
/ VOLUME: 10TH WORLD CONGRESS ON ANIMAL
/ VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
/ ISSUE: PROGRAMME AND ABSTRACTS
/ PAGES: 104
/ DATE: 3-8 NOV 1991
/
US-08-657-163A-1
/
Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKANDPTPLMIKTE 15
DB 1 LKANDPTPLMIKTE 15

RESULT 3
US-08-657-163A-2
/ Sequence 2, Application US/08657163A
/ Patent No. 574449
/ GENERAL INFORMATION:
/ APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
/ TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
/ TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR
/ TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BINIE V. LIPPS
/ STREET: 4509 MIMOSA DR.
/ CITY: BELLAIRE
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77401
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
/ COMPUTER: IBM COMPATIBLE
/ OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
/ SOFTWARE: MS WORD 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/657,163A
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/310,340
/ FILING DATE: 22 SEPTEMBER 1994
/ CLASSIFICATION: 514

```

APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPL 10
Db 1 LKAMDPTPL 10

RESULT 4
US-08-602-999A-444
Sequence 444, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-444

LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-444

Query Match 44.0%; Score 37; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 5 RALPPTPL 13

RESULT 5
US-09-500-124-444
Sequence 444, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-444

Query Match 44.0%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 5 RALPPTPL 13

RESULT 6
US-08-336-343A-31
; Sequence 31, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TRILEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-336-343A-31

Query Match 38.1%; Score 32; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMPTPPL 10
DB 3 KMPFPRPL 11

RESULT 7
US-08-652-877-31
; Sequence 31, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akersstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Raak, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalim, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3808
; TELEFAX: 610-454-3816
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-652-877-31

Query Match 38.1%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMPTPPL 10
DB 3 KMPFPRPL 11

RESULT 8
US-08-476-515A-31
; Sequence 31, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akersstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Raak, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalim, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (patentin)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA: NO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-476-515A-31

Query Match 38.1%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 3 KMPPTPL 11

RESULT 9
US-08-602-999A-252
Sequence 252, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUTILAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-252

Query Match 38.1%; Score 32; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 4 KMPPTPL 12

RESULT 10
US-09-500-124-252
Sequence 252, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUTILAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-252

Query Match 38.1%; Score 32; DB 4; Length 12;
 Best Local Similarity 66.7%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
 Db 4 KMPMPRPL 12

RESULT 11
 US-09-268-992-70

; Sequence 70, Application US/09268992

; Patent No. 6342351

; GENERAL INFORMATION:

; APPLICANT: Chen, H.

; APPLICANT: Freimer, N.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; FILE REFERENCE: 7853-138

; CURRENT APPLICATION NUMBER: US/09/268,992

; EARLIER FILING DATE: 1999-03-16

; EARLIER APPLICATION NUMBER: 09/236,134

; EARLIER FILING DATE: 1999-01-22

; EARLIER APPLICATION NUMBER: 60/106,056

; EARLIER FILING DATE: 1998-10-28

; EARLIER APPLICATION NUMBER: 60/088,312

; EARLIER FILING DATE: 1998-06-05

; EARLIER APPLICATION NUMBER: 60/078,044

; EARLIER FILING DATE: 1998-03-16

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 70

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-268-992-70

Query Match 38.1%; Score 32; DB 3; Length 14;
 Best Local Similarity 80.0%; Pred. No. 95;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPLM 11
 Db 7 TPLM 11

RESULT 12

US-09-657-474-70

; Sequence 70, Application US/09657474

; Patent No. 6399762

; GENERAL INFORMATION:

; APPLICANT: Chen, H.

; APPLICANT: Freimer, N.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; FILE REFERENCE: 7853-138

; CURRENT APPLICATION NUMBER: US/09/657,474

; EARLIER FILING DATE: 2000-09-07

; EARLIER APPLICATION NUMBER: 09/268,992

; EARLIER FILING DATE: 1999-03-16

; EARLIER APPLICATION NUMBER: 60/236,134

; EARLIER FILING DATE: 1999-01-22

; EARLIER APPLICATION NUMBER: 60/106,056

; EARLIER FILING DATE: 1998-10-28

; EARLIER APPLICATION NUMBER: 60/088,312

; EARLIER FILING DATE: 1998-06-05

; EARLIER APPLICATION NUMBER: 60/078,044

; EARLIER FILING DATE: 1998-03-16

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 70

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-657-474-70

Query Match 38.1%; Score 32; DB 3; Length 14;
 Best Local Similarity 80.0%; Pred. No. 95;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPLM 11
 Db 7 TPLM 11

RESULT 13

US-09-845-583A-13

; Sequence 13, Application US/09845583A

; Patent No. 6635616

; GENERAL INFORMATION:

; APPLICANT: Burgess, Robert

; APPLICANT: Brunken, William Joseph

; APPLICANT: Champiaud, Marie-France

; APPLICANT: Hunter, Dale

; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF

; FILE REFERENCE: 10287-05601

; CURRENT APPLICATION NUMBER: US/09/845,583A

; EARLIER FILING DATE: 2001-04-30

; EARLIER APPLICATION NUMBER: US 60/200,863

; EARLIER FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-845-583A-13

Query Match 38.1%; Score 32; DB 4; Length 14;
 Best Local Similarity 50.0%; Pred. No. 95;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AMDPTPLM 12
 Db 2 ANSPRPLM 11

RESULT 14

US-09-547-693-160

; Sequence 160, Application US/09547693

; Patent No. 6639050

; GENERAL INFORMATION:

; APPLICANT: Kieliszewski, Marcia

; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich

; FILE REFERENCE: OHU-04089

; CURRENT APPLICATION NUMBER: US/09/547,693

; EARLIER FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 236

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 160

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial/Unknown

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Synthetic

; NAME/KEY: SITE

; LOCATION: (3)..(3)

; OTHER INFORMATION: The Proline at this position is a hydroxyproline.

; NAME/KEY: SITE

; LOCATION: (7)..(7)

; OTHER INFORMATION: The Proline at this position is a hydroxyproline.

; NAME/KEY: SITE

; LOCATION: (9)..(10)

; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

NAME/KEY: SITE
LOCATION: (14)..(14)
OTHER INFORMATION: The proline at this position is a hydroxyproline:
US-09-547-693-160

Query Match 38.1%; Score 32; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
DB 4 SLPTPL 11

RESULT 15
US-09-232-446B-11
Sequence 11, Application US/09232446B
Patent No. 6228647
GENERAL INFORMATION:
APPLICANT: Voytas, Daniel F.
APPLICANT: Gal, Xiaowu
TITLE OF INVENTION: Transposable Element Protein that Directs DNA
FILE REFERENCE: 2-98
CURRENT APPLICATION NUMBER: US/09/232.446B
CURRENT FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 60/071,383
PRIOR FILING DATE: 1998-01-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
US-09-232-446B-11

Query Match 36.9%; Score 31; DB 3; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMDPTPL 9
DB 4 SLPTPL 10

Search completed: January 6, 2005, 11:17:35
Job time : 37 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 11:17:41 ; Search time 38 Seconds
(without alignments)
30.384 Million cell updates/sec

Title: US-10-047-945-4

Sequence: 1 LKAMPPTPLWT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

.Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	39.1	7	2 A61081	tryptophyllin, bas
2	27	39.1	10	2 A36454	trypsin-modulating
3	24	34.8	8	2 S21288	lectin - potato (f
4	23	33.3	7	4 A58725	vitrotoxin - decto
5	21	30.4	10	2 C35389	urease (EC 3.5.1.5
6	21	30.4	10	2 B59272	peptide-N4-(N-acet
7	21	30.4	10	2 S39030	lysoyl-bradykinin -
8	21	30.4	11	1 XAVIBH	bradykinin-potent
9	20	29.0	5	2 B60274	major protein anti
10	20	29.0	8	2 S10783	enamelin f - bovin
11	20	29.0	8	2 A39308	glycine reductase
12	20	29.0	12	1 UTUGO	tremorogen A-10 -
13	20	29.0	12	1 PN0663	dystrophin-associa
14	19	27.5	9	2 B30572	T-cell receptor be
15	19	27.5	9	2 A60108	exotoxin A - Strep
16	19	27.5	9	2 S26508	collagen alpha 2(V
17	19	27.5	10	2 C30572	T-cell receptor be
18	19	27.5	11	2 D45900	complement C3b rec
19	18	26.1	4	2 I51049	metallothionein-A
20	18	26.1	8	2 S71919	alcohol dehydrogen
21	18	26.1	10	2 PC2171	triacylglycerol 11
22	18	26.1	10	2 A61007	hemelin (EC 3.4.-
23	18	26.1	11	2 C61487	seed protein wa-18
24	18	26.1	12	2 A49033	T-cell receptor de
25	18	26.1	12	2 JQ2308	hypothetical 1.4K
26	18	26.1	12	2 JQ2318	hypothetical 1.4K
27	18	26.1	12	2 I58273	thyroglobulin - ra
28	18	26.1	12	2 S07436	techkinin - Afric
29	17	24.6	7	2 S09652	hypothetical prote

30	17	24.6	8	2 JS0317	leucokinin VII - M
31	17	24.6	10	2 A61218	alpha-gliadin 4Ha
32	17	24.6	10	2 B61218	alpha-gliadin 6Ha
33	17	24.6	11	2 P00231	beta-glucosidase (
34	17	24.6	12	2 A26093	microbial collagen
35	17	24.6	12	2 S70337	napin small chain
36	17	24.6	12	2 PH1587	Ig H chain V-D-J r
37	17	24.6	12	2 PH1611	Ig H chain V-D-J r
38	17	24.6	12	2 PN0046	ATP synthase D cha
39	17	24.6	12	2 S71380	leibetin I isoform
40	16	23.2	5	2 B37988	acid proteinase 11
41	16	23.2	8	2 S10596	adipokinetic hormo
42	16	23.2	8	2 S19288	acylase - Kluyvera
43	16	23.2	8	2 A31570	angiotensin-conver
44	16	23.2	9	2 I58350	gene c-mpl protein
45	16	23.2	9	2 D48186	ATPase R1 subunit

ALIGNMENTS

RESULT 1

A61081
C/Species: Phyllomedusa rohdei (Rohde's leaf frog)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 18-Aug-2000
C/Accession: A61081
R/Montecluchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
Int. J. Pept. Protein Res. 33, 391-395, 1989
A/Title: Isolation, structure determination and synthesis of a novel tryptophan-contain
A/Reference number: A61081
A/Accession: A61081
A/Molecule type: protein
A/Residues: 1-7 <MON>
C/Comment: The biological activity of this peptide was not determined.
C/Superfamily: unassigned animal peptides
C/Keyword: amidated carboxyl end; hydroxyproline; skin
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
F/7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 39.1%; Score 27; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLWI 12
Db 2 PPSWI 6

RESULT 2

A36454
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #ext_change 09-Jul-2004
C/Accession: A36454; A61630
R/Borovsky, D.; Carlsson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A/Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme b
A/Reference number: A36454; MWID:90367888; PMID:2394318
A/Accession: A36454
A/Molecule type: protein
A/Residues: 1-10 <BOK>
A/Cross-references: UNIPROT:P19425
R/Borovsky, D.; Carlsson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A/Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A/Reference number: A61630; MWID:93357794; PMID:8353526
A/Accession: A61630
A/Molecule type: protein
A/Residues: 1-10 <BOK>
A/Note: none of the amino acids is modified
C/Function:
A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut e

C:Keywords: hormone

Query Match 39.1%; Score 27; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
| | |
| | |
DB 2 DPAP 6

RESULT 3

S21288

lectin - potato (fragment)

C:Species: Solanum tuberosum (potato)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C:Accession: S21288

R:Miller, D.V.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization

A:Reference number: S21288; MUID:92272683; PMID:1590771

A:Accession: S21288

A:Molecule type: protein

A:Residues: 1-8 <ML>

A:Cross-references: UNIPROT:Q7M1V6

A:Experimental source: var. Ulster Sceptre

C:Function: A:Description: may be involved in defence mechanism of the plant

C:Keywords: hydroxyproline, lectin

Query Match

Best Local Similarity 34.8%; Score 24; DB 2; Length 8;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDTPP 9
| | |
| | |
DB 2 ASTPSP 8

RESULT 4

A58725

Vitrotoxin - destroying angel

C:Species: Amanita virosa (destroying angel)

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: A58725

R:Paulstich, H.; Buku, A.; Bodenmuller, H.; Wieland, T.

Biochemistry 19, 334-343, 1980

A:Title: Vitrotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.

A:Reference number: A58725; MUID:6893271; PMID:6893271

A:Accession: A58725

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <FAU>

C:Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide

F:1-7/Cross-link: cyclopeptide (Val-Leu) #status experimental

F:2/Modified site: D-threonine (Thr) #status experimental

F:3/Modified site: D-serine (Ser) #status experimental

F:4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental

F:6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental

F:7/Modified site: 4,5-dihydroxytryptophan (Leu) #status experimental

Query Match

Best Local Similarity 33.3%; Score 23; DB 4; Length 7;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TPPLMT 12
| | |
| | |
DB 2 TSPAWL 7

RESULT 5

C35389

urease (EC 3.5.1.5) 6K chain - Morganelia morgani (fragment)

C:Species: Morganelia morgani

C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004

C:Accession: C35389

R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A:Title: Morganelia morgani urease: purification, characterization, and isolation of ge

A:Reference number: A35389; MUID:90264298; PMID:2345135

A:Accession: C35389

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <HUA>

A:Cross-references: UNIPROT:P17339

C:Keywords: hydrolase

Query Match

Best Local Similarity 30.4%; Score 21; DB 2; Length 10;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
| | |
| | |
DB 1 MQLTPP 6

RESULT 6

B59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -

N:Alternate names: peptide N-glycosidase

C:Species: Prunus dulcis var. sativa (sweet almond)

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: B59272

R:Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Bur. J. Biochem. 252, 118-123, 1998

A:Title: Characterization of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A

A:Reference number: A59272; MUID:8618894; PMID:9523720

A:Accession: B59272

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <ALT>

A:Cross-references: UNIPROT:P81898

C:Keywords: hydrolase

Query Match

Best Local Similarity 30.4%; Score 21; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
| | |
| | |
DB 1 EPTP 4

RESULT 7

S39030

lysy1-bradykinin - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004

C:Accession: S39030

R:Conlon, J.M.; Olson, K.R.

FEBS Lett. 334, 75-78, 1993

A:Title: Purification of a vasoactive peptide related to lysy1-bradykinin from trout pla

A:Reference number: S39030; MUID:94039817; PMID:8224232

A:Accession: S39030

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CON>

A:Cross-references: UNIPROT:Q9PRZ1

Query Match

Best Local Similarity 30.4%; Score 21; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLW 11
| | |
| | |
DB 3 PPGW 6

RESULT 8

XAVIBH

bradykinin-potentiating peptide - halys viper

N:Alternate names: BPP

C:Species: Agkistrodon halys (halys viper)

C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004

C/Accession: J00002

R:Chl, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

P:Peptides 6, 339-342, 1985

A>Title: Structure-function studies on the bradykinin potentiating peptide from Chinese

A:Reference number: J00002; PMID:86177022; PMID:3008123

A:Accession: J00002

A:Molecule type: protein

A:Residues: 1-11 <CHI>

A:Cross-references: UNIPROT:P04562

C:Comment: Because this peptide both inhibits the activity of the angiotensin-converting

C:Superfamily: bradykinin-potentiating enzyme inhibitor; antihypertensive; bradykinin; pyrog

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 30.4%; Score 21; DB 1; Length 11;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPPL 10

DB 5 PCGPI 9

RESULT 9

B60274

Major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C/Accession: B60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

P:Infect. Immun. 59, 372-382, 1991

A>Title: Isolation and partial characterization of major protein antigens in the culture

A:Reference number: A60274; PMID:9109989; PMID:1898899

A:Accession: B60274

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <NAG>

Query Match

Best Local Similarity 29.0%; Score 20; DB 2; Length 5;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTP 8

DB 1 DPAP 4

RESULT 10

S10783

enamelin f - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C/Accession: S10783

R:Strawich, E.; Glincher, M.J.

P:Bur. J. Biochem. 191, 47-56, 1990

A>Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu

A:Reference number: S10780; PMID:9033661; PMID:2379503

A:Accession: S10783

A:Molecule type: protein

A:Residues: 1-8 <STR>

C:Keywords: enamel; phosphoprotein

Query Match

Best Local Similarity 29.0%; Score 20; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9

DB 2 PLPP 5

RESULT 11

A93308

glycine reductase (EC 1.4.99.-) sulhydryl protein C, alpha chain - Clostridium sticklandii

C:Species: Clostridium sticklandii

C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004

C/Accession: A93308

R:Schadman, T.C.; Davis, J.N.

P:U. Biol. Chem. 266, 22147-22153, 1991

A>Title: Glycine reductase protein C. Properties and characterization of its role in th

A:Reference number: A93308; PMID:92042141; PMID:1939235

A:Accession: A93308

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STR>

A:Cross-references: UNIPROT:Q7M0L0

C:Function:

C:Keywords: ATP; oxidoreductase

Query Match

Best Local Similarity 29.0%; Score 20; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLM 11

DB 3 PVLW 6

RESULT 12

JTRUG0

tremetogen A-10 - jelly fungus (Tremella mesenterica)

C:Species: Tremella mesenterica

C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

C/Accession: A01642; A61313

R:Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.

P:Science 212, 1525-1527, 1981

A>Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-

A:Reference number: A94256

A:Accession: A01642

A:Molecule type: protein

A:Residues: 1-12 <SAK1>

A:Note: the farnesyl may instead be (2E,6E,10E)-12-hydroxyfarnesyl

R:Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.

P:Agric. Biol. Chem. 42, 1301-1302, 1978

A>Title: Amino acid sequence of tremetogen A-10, a peptidic hormone, inducing conjugati

A:Reference number: A61313

A:Accession: A61313

A:Molecule type: protein

A:Residues: 1-12 <SAK2>

C:Comment: Tremetogen A-10 is produced by the A mating-type cells and induces formation

C:Superfamily: tremetogen a-13

C:Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; phero

F:/2/Binding site: farnesyl (Cys) (covalent) #status experimental

F:/2/Modified site: methyl ester carboxyl end (Cys) #status experimental

Query Match

Best Local Similarity 29.0%; Score 20; DB 1; Length 12;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9

DB 3 DPAP 7

RESULT 13

PN0663

Search completed: January 6, 2005, 11:27:11
 Job time : 39 secs

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C/Accession: FN0663
 R/Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A/Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
 A/Reference number: FN0662; MUID:94156881; PMID:8113213
 A/Accession: FN0663
 A/Molecule type: protein
 A/Residues: 1-12 <YOS>
 C/Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C/Keywords: glycoprotein; skeletal muscle

Query Match 29.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
 |||
 Db 3 PLPP 6

RESULT 14

B30572
 T-cell receptor beta chain C region (CRTB29) - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
 C/Accession: B30572
 R/Williams, C.B.; Gutman, G.A.
 J. Immunol. 142, 1027-1035, 1989
 A/Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utilization
 A/Reference number: A30563; MUID:89110038; PMID:2563271
 A/Accession: B30572
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-9 <WIL>
 C/Keywords: T-cell receptor

Query Match 27.5%; Score 19; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPP 9
 |||
 Db 7 TPP 9

RESULT 15

A60108
 exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)
 N/Alternate names: blastogen A; scarlet fever toxin
 C/Species: Streptococcus pyogenes
 C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
 C/Accession: A60108
 R/Schlevert, P.M.; Gray, E.D.
 Infect. Immun. 57, 1865-1867, 1989
 A/Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast
 A/Reference number: A60108; MUID:89254013; PMID:2498210
 A/Accession: A60108
 A/Molecule type: protein
 A/Residues: 1-9 <SCH>
 A/Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNIF
 C/Keywords: exotoxin

Query Match 27.5%; Score 19; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTP 8
 |||
 Db 2 DPDP 5

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 11:17:01; Search time 188 Seconds

(without alignments)
36.726 Million cell updates/sec

Title: US-10-047-945-4

Sequence: 1 LKAMPPTPLMT 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	39.1	7	1	TPFY_PACDA
2	27	39.1	10	1	TPFY_PACDA
3	26	37.7	11	1	TPFY_PACDA
4	25	36.2	12	2	Q9UCR1
5	25	36.2	12	2	Q6X7V1
6	25	36.2	12	2	Q8KZ86
7	24	34.8	12	2	AAP79619
8	23	33.3	10	2	Q7M1V6
9	23	33.3	10	2	Q76MK5
10	23	33.3	11	2	BAB87160
11	23	33.3	11	2	Q8IVG8
12	22	31.9	11	2	CAA33464
13	22	31.9	11	2	Q8MAZ1
14	22	31.9	11	2	Q8MAZ3
15	22	31.9	11	2	Q8MB39
16	22	31.9	11	2	Q8MB58
17	22	31.9	11	2	Q8MB77
18	22	31.9	11	2	Q8MB79
19	22	31.9	11	2	Q8MB97
20	21	30.4	6	1	Q8MBE1
21	21	30.4	9	2	Q9H326
22	21	30.4	9	2	Q6SP94
23	21	30.4	9	2	Q99193
24	21	30.4	9	2	Q9PRJ4
25	21	30.4	9	2	AAR20844
26	21	30.4	10	1	BRK_ONCR1
27	21	30.4	10	1	URE3_MORMO
28	21	30.4	10	1	P81898
29	21	30.4	11	1	BPP_AGKAP
30	21	30.4	11	2	Q77896
31	21	30.4	12	2	Q47251

32	20	29.0	7	1	UP04_MOUSE
33	20	29.0	8	2	Q7M010
34	20	29.0	10	2	Q91WZ3
35	20	29.0	10	2	Q75595
36	20	29.0	10	2	AAP76567
37	20	29.0	11	2	Q9HCN5
38	20	29.0	12	1	TA10_TREME
39	20	29.0	12	2	Q9BZ49
40	20	29.0	12	2	Q7YNG6
41	19	27.5	8	2	Q6LDP8
42	19	27.5	8	2	Q9ERT6
43	19	27.5	8	2	Q9ERT7
44	19	27.5	8	2	Q9ERT8
45	19	27.5	8	2	AAA26011

ALIGNMENTS

RESULT 1	ID	TPFY_PACDA	STANDARD	PRT	7 AA
AC P83455;					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Trypophyllin-1 (Pdt-1)					
OS Pachymedusa daemnicolor (Giant Mexican leaf frog)					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;					
OC Phyllomedusinae; Pachymedusa.					
NCBI_TaxId=75988;					
RN [1]					
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.					
RC TISSUE-Skin secretion;					
RT Chen T.B., Orr D.F., Shaw C.;					
RT "Pachymedusa daemnicolor tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA."					
RL Submitted (SEP-2002) to Swiss-Prot.					
CC -!- FUNCTION: Myosin. Has selective relaxing activity on vascular smooth muscle.					
CC -!- SUBCELLULAR LOCATION: Secreted.					
CC -!- TISSUE SPECIFICITY: Skin.					
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.					
DR GO; GO:0005576; C:extracellular; NAS.					
DR GO; GO:0045986; P:negative regulation of smooth muscle contractility; NAS.					
KW Amidation; Amphibian defense peptide; Direct protein sequencing;					
KW Hydroxylation.					
FT MOD RES 3					
FT MOD RES 7					
FT MOD RES 7					
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;					
Query Match					
Best Local Similarity					
Matches					
3; Conservative					
1; Mismatches					
1; Indels					
0; Gaps					
0;					
RESULT 2					
ID TMOF_AEDAR					
AC P19425;					
DT 01-NOV-1990 (Rel. 16, Created)					
DT 01-NOV-1990 (Rel. 16, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Tryptin-modulating oostatic factor (TMOF) (OOSH).					
OS Aedes aegypti (Yellowfever mosquito).					
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxId=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=9036788; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
RT enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
CC and stops at 56 hrs.
CC PIR: A36454; A36454.
KM Direct protein sequencing; Hormone.
FT DOMAIN 3 10 Poly-Pro.
FT VARIANT 1 2 YD->DX (IN TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 39.1%; Score 27; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAP 6

RESULT 3
Q9UCR1 PRELIMINARY; PRT; 11 AA.
ID Q9UCR1;
AC Q9UCR1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=9219337; PubMed=1733949;
RA Stracke M.L., Kutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schifmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autocatalin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 37.7%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLWI 12
DB 4 PLWI 7

RESULT 4
O6X7VL PRELIMINARY; PRT; 12 AA.
ID O6X7VL;
AC O6X7VL;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Insulin-like factor 3 (Fragment).
GN Name=INSL3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22929740; PubMed=12890727;
RA Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.;
RT "Isolation and expression analysis of the canine insulin-like factor 3
RT gene.";
RL Biol. Reprod. 69:1658-1664(2003).
DR EMBL: AY251015; AAP79619.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPPTPLW 11
DB 1 MSPRPLW 8

RESULT 5
Q8KZ86 PRELIMINARY; PRT; 12 AA.
ID Q8KZ86;
AC Q8KZ86;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Class I Integrin DNA integrase (Fragment).
GN Name=Int11;
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxId=470;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22270987; PubMed=12384388;
RA Gombac F., Riccio M.L., Rosolinski G.M., Lagacolla C., Tonin E.,
RA Monti-Bragadin C., Lavenia A., Dolzani L.;
RT "Molecular characterization of integrins in epidemiologically
RT unrelated clinical isolates of Acinetobacter baumannii from Italian
RT hospitals reveals a limited diversity of gene cassette arrays.";
RL Antimicrob. Agents Chemother. 46:3665-3668(2002).
DR EMBL: AJ313334; CAC85941.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMPDPTPL 10
DB 4 ATAPLPL 11

RESULT 6
AAP79619 PRELIMINARY; PRT; 12 AA.
ID AAP79619;
AC AAP79619;
DT 02-MAR-2004 (TREMBLrel. 27, Created)


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DT 02-MAR-2004 (Tremblrel. 27, last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, last annotation update)
DE Insulin-like factor 3 (Fragment).
GN INS13.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1289727;
RA Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.;
RT "Isolation and Expression Analysis of the Canine Insulin-Like Factor 3
RL Gene."
RL EMBL; AY251015; AAF79619.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPTPLW 11
DB 1 MSRPPLAW 8

RESULT 7
Q7M1V6 PRELIMINARY; PRT; 8 AA.
AC Q7M1V6;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Lectin (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RA Miller D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
RA Bolwell G.P.;
RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
RT Characterization, immunolocalization and effects of wounding."
RL Biochem. J. 283:813-821(1992).
DR PIR; S21288; S21288. 1
FT NON TER 1 8
SQ SEQUENCE 8 AA; 771 MW; C37775A771BSBD4A CRC64;

Query Match 34.8%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPP 9
DB 2 ASTPSP 8

RESULT 8
Q76MK5 PRELIMINARY; PRT; 10 AA.
AC Q76MK5;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, last annotation update)
DE ATPase subunit 8 (Fragment).
GN Name=ATPase 8;
OS Eurypharynx pelicanoides (pelican eel).
OS Mitochondrion.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RL scale gene rearrangements originated within the eels."
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBD databases.
DR EMBL; AB046487; BAB87160.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KM Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
DB 4 LDSP 8

RESULT 9
BAB87160 PRELIMINARY; PRT; 10 AA.
AC BAB87160;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, last annotation update)
DE ATPase subunit 8 (Fragment).
GN ATPase 8.
OS Eurypharynx pelicanoides (pelican eel).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
RT Scale Gene Rearrangements Originated Within the Eels."
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D;
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBD databases.
DR EMBL; AB046487; BAB87160.1; -.
KM Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTP 8
DB 4 LDSP 8

RESULT 10
Q81VG8

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ID O81VG8 PRELIMINARY; PRT; 11 AA.
AC O81VG8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Low density lipoprotein receptor related protein 1 (lipoprotein
DE receptor-related protein) (Fragment).
GN Name=LRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butcheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Glaeser C.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Schultz S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=9089395; PubMed=2597675;
RA Kuett H.C., Herz J., Stanley K.K.;
RT "Structure of the low-density lipoprotein receptor-related protein
RT (LRP) Promoter.";
RL Biochim. Biophys. Acta 1009:229-236 (1989).
DR EMBL; Y18524; CAD57169.1; -.
DR EMBL; X15424; CA433464.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Lipoprotein; Receptor.
FT NON TER 11
SQ SEQUENCE 11 AA; 1221 MW; 373D041B27273777 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPPL 10
DB 3 TPPL 6

RESULT 11
CA433464 PRELIMINARY; PRT; 11 AA.
AC CA433464;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Lipoprotein receptor-related protein (Fragment).
GN LRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butcheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RA Kuett H.C., Herz J., Stanley K.K.;
RT "Structure of the low-density lipoprotein receptor-related protein
RT (LRP) Promoter.";
RL Biochim. Biophys. Acta 1009:229-236 (1989).
DR EMBL; X15424; CA433464.1; -.
KM Receptor.
FT NON TER 11
SQ SEQUENCE 11 AA; 1221 MW; 373D041B27273777 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPPL 10
DB 3 TPPL 6

RESULT 12
O8MAZ1 PRELIMINARY; PRT; 11 AA.
AC O8MAZ1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PabJ (Fragment).
GN Name=pabJ;
OS Maripa paniculata.
OX Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197411;
RN 11
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Oimstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 89:1510-1522 (2002).
DR EMBL; AY100937; AA055869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON TER 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLW 11
DB 9 PLW 11

RESULT 13
O8MAZ3 PRELIMINARY; PRT; 11 AA.
AC O8MAZ3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PabJ (Fragment).
GN Name=pabJ;
OS Maripa repens.
OX Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Convolvulaceae; Maripa.
OX NCBI_TaxID=197412;
RN 11
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Oimstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 89:1510-1522 (2002).
DR EMBL; AY100936; AA055865.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON TER 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 9 PLW 11
 |||
 Db 9 PLW 11

RESULT 14

Q8MB39 PRELIMINARY; PRT; 11 AA.
 AC Q8MB39;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Pobj (Fragment).
 GN Name=pobj;
 OS Wilsontia humilis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Convolvulaceae; Wilsontia.
 OX NCBI_TaxID=197481;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 lineages based on DNA sequences of multiple chloroplast loci."
 RL Am. J. Bot. 89:1510-1522(2002).
 DR EMBL; AY100914; AA055777.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLW 11
 |||
 Db 9 PLW 11

RESULT 15

Q8MB58 PRELIMINARY; PRT; 11 AA.
 ID Q8MB58;
 AC Q8MB58;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Pobj (Fragment).
 GN Name=pobj;
 OS Seddera hirsuta.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Convolvulaceae; Seddera.
 OX NCBI_TaxID=197444;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 lineages based on DNA sequences of multiple chloroplast loci."
 RL Am. J. Bot. 89:1510-1522(2002).
 DR EMBL; AY100905; AA055743.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLW 11
 |||
 Db 9 PLW 11

Search completed: January 6, 2005, 11:26:28
 Job time : 191 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 11:09:21 ; Search time 153 Seconds
(without alignments)
28.136 Million cell updates/sec

Title: US-10-047-945-4
Perfect score: 69
Sequence: 1 LKAMDPTPLPMT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues
Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	12	7	ABR12046
2	65	94.2	11	7	ABR12234
3	54	78.3	10	2	AAW53843
4	54	78.3	10	7	ABR12234
5	50	72.5	9	7	ABR12234
6	43	62.3	8	7	ABR12234
7	41	59.4	9	6	ABR12621
8	41	59.4	9	6	ABR12017
9	41	59.4	9	6	ABR12854
10	41	59.4	10	6	ABR12743
11	41	59.4	10	6	ABR11875
12	41	59.4	10	6	ABR12121
13	41	59.4	10	6	ABR12948
14	41	59.4	10	6	ABR12106
15	41	59.4	10	6	ABR12294
16	41	59.4	10	6	ABR12738
17	38	55.1	9	2	AAW21252
18	37	53.6	9	6	ABR11778
19	37	53.6	9	6	ABR12206
20	37	53.6	10	6	ABR12924
21	37	53.6	10	8	AD064358
22	36	52.2	9	6	ABR12770
23	36	52.2	9	6	ABR12969
24	36	52.2	9	6	ABR12458
25	36	52.2	9	6	ABR12601

26	36	52.2	9	6	ABR12046	Abri12046 Human can
27	36	52.2	9	6	ABR12234	Abri12234 Human can
28	36	52.2	9	8	AD072393	Ado72393 Human 213
29	36	52.2	9	8	AD072483	Ado72483 Human 213
30	36	52.2	9	8	AD072536	Ado72536 Human 213
31	36	52.2	9	8	AD072664	Ado72664 Human 213
32	36	52.2	9	8	AD072353	Ado72353 Human 213
33	36	52.2	9	8	AD072482	Ado72482 Human 213
34	36	52.2	9	8	AD064670	Ado64670 Human 213
35	36	52.2	9	8	AD065216	Ado65216 Human 213
36	36	52.2	9	8	AD067376	Ado67376 Human 213
37	36	52.2	9	8	AD072238	Ado72238 Human 213
38	36	52.2	9	8	AD064109	Ado64109 Human 213
39	36	52.2	9	8	AD065758	Ado65758 Human 213
40	36	52.2	9	8	AD067387	Ado67387 Human 213
41	36	52.2	9	8	AD072320	Ado72320 Human 213
42	36	52.2	9	8	AD072329	Ado72329 Human 213
43	36	52.2	9	8	AD064657	Ado64657 Human 213
44	36	52.2	9	8	AD065214	Ado65214 Human 213
45	36	52.2	9	8	AD065785	Ado65785 Human 213

ALIGNMENTS

RESULT 1	ABR12046	standard; peptide; 12 AA.
ID	ABR12046	
AC	ABR12046	
XX	ABR12046	
DT	06-NOV-2003	(first entry)
DE	Synthetic LTNF, LT-12.	
KM	Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;	
KM	IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;	
KM	ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;	
KM	SLE; rheumatoid arthritis; Sjogren's syndrome; Kellie's syndrome;	
KM	Graves' disease; Addison's disease; Hodgkin's disease; depression;	
KM	Saliva; ELISA.	
OS	Synthetic.	
XX	WO2003060471-A2.	
XX	24-JUL-2003.	
PF	14-JAN-2003; 2003WO-US001044.	
XX	14-JAN-2003; 2002US-00047945.	
XX	(LIPF/) LIPPS B V.	
PA	(LIPF/) LIPPS F W.	
XX	Lipps BV, Lipps FW;	
PT	WP1; 2003-636703/60.	
XX	Assaying a human endogenous protein (e.g. IGF, nerve growth factor,	
PT	insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.	
PT	asthma or diabetes, by employing an ELISA on a saliva sample from a	
PT	patient.	
XX	Claim 7; Page 4; 24pp; English.	
CC	The sequences given in ABR12046-28 represent lethal toxin neutralising	
CC	factor (LTNF) peptides which may be used for reducing elevated levels of	
CC	serum proteins selected from immunoglobulin E (IgE), nerve growth factor	
CC	(NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In	
CC	particular, the methods of the invention are useful for diagnosing and	
CC	treating conditions with elevated serum IGF levels, e.g. asthma,	
CC	diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid	

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 12 AA;

Query Match Best Local Similarity 100.0%; Score 69; DB 7; Length 12;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 12
 DB 1 LKAMDPTPLMT 12

RESULT 2
 ID ABB80226 standard; peptide; 11 AA.
 AC ABB80226;
 DT 06-NOV-2003 (first entry)

XX Synthetic LTNF, LT-11.
 DE

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.

XX Synthetic.

XX WO2003060471-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001044.

XX 14-JAN-2002; 2002US-00047945.

XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.

XX LIPPS BV, LIPPS FW;
 PI

XX WPI, 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by

CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 11 AA;

Query Match Best Local Similarity 94.2%; Score 65; DB 7; Length 11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 11
 DB 1 LKAMDPTPLMT 11

RESULT 3
 ID AAM53843 standard; peptide; 10 AA.
 AC AAM53843;
 DT 08-JUL-1998 (first entry)

XX N-terminus of opossum LTNF.
 DE

XX LTNF, lethal toxin neutralising factor; opossum; envenomation; therapy;
 KM anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KM sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KM histamine reaction treatment.

XX Didelphis virginiana.

XX US5744449-A.

XX 28-APR-1998.

XX 03-JUN-1996; 96US-00657163.

XX 10-MAY-1993; 93US-00058387.

XX 22-SEP-1994; 94US-00310340.

XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.

XX LIPPS BV, LIPPS FW;
 PI

XX WPI, 1998-271106/24.

XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.

XX Claim 7; Col 11; 11pp; English.

XX This sequence represents the peptide of the invention. It is a lethal
 CC Toxin Neutralising Factor (LTNP) moiety from a 66 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX Sequence 10 AA;

Query Match 78.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
 |||||
 1 LKAMDPTPPL 10

RESULT 4
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 XX
 AC ABB80222;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-10.
 XX

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX

14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX

(LIRP/) LIRPS B V.
 PA (LIRP/) LIRPS F W.
 XX

LIRPS BV, LIRPS FW;
 PI
 DR WPI; 2003-636703/60.
 XX

Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX

Claim 7; Page 3; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

Sequence 10 AA;

Query Match 78.3%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
 |||||
 1 LKAMDPTPPL 10

RESULT 5
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 AC ABB80227;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-9.
 XX

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX

14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX

(LIRP/) LIRPS B V.
 PA (LIRP/) LIRPS F W.
 XX

LIRPS BV, LIRPS FW;
 PI
 DR WPI; 2003-636703/60.
 XX

Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

Sequence 9 AA;

Query Match 72.5%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 9
 |||||

Db 1 LKAMPPTP 9

RESULT 6

ABR80228 standard; peptide; 8 AA.

AC ABR80228;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNF, LT-8.

XX Lethal toxin neutralizing factor; LTNF; serum protein; immunoglobulin E;
 KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.

XX Synthetic.

PN WO2003060471-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPP/) LIPPS B V.
 (LIPP/) LIPPS F W.

PI Lippe BV, Lippe FW;

XX WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 7; Page 4; 24pp; English.

XX The sequences given in ABR80222-28 represent lethal toxin neutralizing
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin B (IGB), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGB levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

Query Match 62.3%; Score 43; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMPPTP 8
 |||||
 1 LKAMPPTP 8

RESULT 7
 ABR12621
 ID ABR12621 standard; peptide; 9 AA.

AC ABR12621;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 156P1D4 HLA peptide #856.

XX Human, cytostatic; vaccine; cancer; immune response; HLA;
 KM human leukocyte antigen.

XX Homo sapiens.

PN WO200283921-A2.

PD 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011654.

PR 10-APR-2001; 2001US-0282739P.
 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

PA (AGEN-) AGENSYS INC.

PI Jakobovits A, Challita-Bid FM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 238; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX Sequence 9 AA;

Query Match 59.4%; Score 41; DB 6; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.7e+06; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLMI 12
 |||||
 1 MDPPTPLMI 9

RESULT 8

ABR12017
 ID ABR12017 standard; peptide; 9 AA.

AC ABR12017;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 156P1D4 HLA peptide #252.

KM Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Rid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 232; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
XX
Query Match 59.4%; Score 41; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPPTPIWI 12
|||:|:
Db 1 MDPSVPIWI 9
XX
RESULT 9
ABR12854
ID ABR12854 standard; peptide; 9 AA.
XX
AC ABR12854;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #1089.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PN 24-OCT-2002.
XX
PD 10-APR-2002; 2002WO-US011654.
PF

XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Rid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 240; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
XX
Query Match 59.4%; Score 41; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPPTPIWI 12
|||:|:
Db 1 MDPSVPIWI 9
XX
RESULT 10
ABR12743
ID ABR12743 standard; peptide; 10 AA.
XX
AC ABR12743;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #978.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PN 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Rid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX

DR WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 239; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 10 AA;
XX
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLMI 12
DB 1 MDPSVPIWI 9
XX
RESULT 11
ABR1875
ID ABR1875 standard; peptide; 10 AA.
XX
AC ABR1875;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #110.
XX
KM Human; cytostatic; vaccine; cancer; immune response; HLA;
KM human leukocyte antigen.
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eld PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
CC New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 231; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and

CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 10 AA;
XX
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLMI 12
DB 2 MDPSVPIWI 10
XX
RESULT 12
ABR12121
ID ABR12121 standard; peptide; 10 AA.
XX
AC ABR12121;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #356.
XX
KM Human; cytostatic; vaccine; cancer; immune response; HLA;
KM human leukocyte antigen.
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eld PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
CC New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 233; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention
XX Sequence 10 AA;

Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLMI 12
| | | : | | |
DB 1 MDPSVPIWI 9

RESULT 13

ABR12948
ID ABR12948 standard; peptide; 10 AA.

AC ABR12948;

XX 19-MAY-2003 (first entry)

DE Human cancer-related protein 156P1D4 HLA peptide #1183.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KM human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

DR New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

PS Claim 13; Page 241; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. CC The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as CC therapeutic, prognostic and diagnostic reagents for cancer. The present CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention

XX Sequence 10 AA;

Query Match 59.4%; Score 41; DB 6; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLMI 12
| | | : | | |

DB 1 MDPSVPIWI 9

RESULT 14

ABR12106
ID ABR12106 standard; peptide; 10 AA.

AC ABR12106;

XX 19-MAY-2003 (first entry)

DE Human cancer-related protein 156P1D4 HLA peptide #341.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KM human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

DR New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

PS Claim 13; Page 233; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. CC The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as CC therapeutic, prognostic and diagnostic reagents for cancer. The present CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention

XX Sequence 10 AA;

Query Match 59.4%; Score 41; DB 6; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLMI 12
| | | : | | |
DB 2 MDPSVPIWI 10

RESULT 15

ABR12294
ID ABR12294 standard; peptide; 10 AA.

AC ABR12294;

XX 19-MAY-2003 (first entry)

```

XX Human cancer-related protein 156PID4 HLA peptide #529.
DE
XX
XX Human, cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US011654.
PF
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Chailita-Bid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
DR
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 235; 1021pp; English.
PS
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 10 AA;
SQ
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPPLWI 12
DB 2 MDPSVPIWI 10

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Search completed: January 6, 2005, 11:23:12
 Job time : 154 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2005, 11:26:37 ; Search time 140 Seconds

(without alignments)
30.906 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69
Sequence: 1 LKAMDPTPLPMT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 210148

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:
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2: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep.*
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20: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	US-10-047-945-4	Sequence 4, App1
2	65	94.2	11	US-10-047-945-5	Sequence 5, App1
3	54	78.3	10	US-10-047-945-1	Sequence 1, App1
4	50	72.5	9	US-10-047-945-6	Sequence 6, App1
5	43	62.3	8	US-10-047-945-7	Sequence 7, App1
6	34	49.3	12	US-10-327-598-735	Sequence 735, App
7	32	46.4	12	US-10-185-815-6	Sequence 6, App1
8	32	46.4	12	US-10-161-791-252	Sequence 252, App
9	32	46.4	12	US-10-116-275-52	Sequence 52, App1
10	31	44.9	9	US-10-611-440-188	Sequence 188, App
11	30	43.5	8	US-10-437-708-168	Sequence 168, App
12	30	43.5	8	US-10-257-199-168	Sequence 168, App
13	30	43.5	10	US-10-190-082-480	Sequence 480, App

14	30	43.5	10	US-10-437-708-165	Sequence 165, App
15	30	43.5	10	US-10-257-199-165	Sequence 165, App
16	30	43.5	12	US-10-225-567A-2288	Sequence 2288, App
17	29	42.0	9	US-09-935-430-7	Sequence 7, App1
18	29	42.0	9	US-10-277-292-7	Sequence 7, App1
19	29	42.0	9	US-10-280-340-7	Sequence 7, App1
20	29	42.0	9	US-10-057-475B-10870	Sequence 10870, A
21	29	42.0	9	US-10-057-475B-10923	Sequence 10923, A
22	29	42.0	9	US-10-057-475B-10929	Sequence 10929, A
23	29	42.0	9	US-10-154-884B-10870	Sequence 10870, A
24	29	42.0	9	US-10-154-884B-10923	Sequence 10923, A
25	29	42.0	9	US-10-154-884B-10929	Sequence 10929, A
26	29	42.0	10	US-09-935-430-74	Sequence 74, App1
27	29	42.0	10	US-09-935-430-619	Sequence 619, App
28	29	42.0	10	US-10-277-292-74	Sequence 74, App1
29	29	42.0	10	US-10-277-292-619	Sequence 619, App1
30	29	42.0	10	US-10-280-340-74	Sequence 74, App1
31	29	42.0	10	US-10-280-340-619	Sequence 619, App1
32	29	42.0	12	US-10-185-815-1	Sequence 1, App1
33	29	42.0	12	US-10-235-175-18	Sequence 18, App1
34	29	42.0	12	US-10-116-275-47	Sequence 47, App1
35	28	40.6	9	US-08-344-824-273	Sequence 273, App
36	28	40.6	10	US-08-344-824-381	Sequence 381, App
37	28	40.6	10	US-09-739-852-7	Sequence 7, App1
38	28	40.6	12	US-10-286-457-136	Sequence 136, App
39	27	39.1	7	US-09-870-480A-8	Sequence 8, App1
40	27	39.1	8	US-09-758-128-20	Sequence 20, App1
41	27	39.1	8	US-09-758-128-23	Sequence 23, App1
42	27	39.1	8	US-09-758-128-26	Sequence 26, App1
43	27	39.1	8	US-09-758-128-29	Sequence 29, App1
44	27	39.1	8	US-09-758-426-20	Sequence 20, App1
45	27	39.1	9	US-09-758-426-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-10-047-945-4
Sequence 4, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
FILE REFERENCE: FMI/PT01505
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 69; DB 14; Length 12;
Best local similarity 100.0%; Pred. No. 0.0011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLPMT 12
|||||
Db 1 LKAMDPTPLPMT 12

RESULT 2

```

US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BIRNIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)E IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match          94.2%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMDPTPLW 11
        |||||
Db       1 LKAMDPTPLW 11

RESULT 3
US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BIRNIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)E IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match          78.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMDPTPL 10
        |||||
Db       1 LKAMDPTPL 10

RESULT 4
US-10-047-945-6
; Sequence 6, Application US/10047945

```

```

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match
Best Local Similarity 100.0%; Score 50; DB 14; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 LKAMDPTP 9
   |||||
Db 1 LKAMDPTP 9

RESULT 5
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match
Best Local Similarity 100.0%; Score 43; DB 14; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 LKAMDPTP 8
   |||||
Db 1 LKAMDPTP 8

RESULT 6
US-10-327-598-735
; Sequence 735, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene

```

```

; APPLICANT: Guo, Hongliang
; APPLICANT: Atiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 735
; LENGTH: 12
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-735

```

```

Query Match      49.3%; Score 34; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 KAMDPTTP 9
Db      1 QSFDPPTP 8

```

```

RESULT 7
US-10-185-815-6
; Sequence 6, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide ligand
US-10-185-815-6

```

```

Query Match      46.4%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 DPTTP 9
Db      5 DPTTP 9

```

```

RESULT 8
US-10-161-791-252
; Sequence 252, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FORTAKES, Dana M.
; APPLICANT: RIDER, James E.

```

```

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-252

```

```

Query Match      46.4%; Score 32; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 KAMDPTTP 10
Db      4 KAMDPTTP 12

```

```

RESULT 9
US-10-116-275-52
; Sequence 52, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Ui
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-52

```

Query Match 46.4%; Score 32; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPL 9
 Db 5 DPTPL 9

RESULT 10

US-10-611-440-188
 ; Sequence 188, Application US/10611440
 ; Publication No. US20040197912A1
 ; GENERAL INFORMATION:

APPLICANT: Berinsteel, Neil
 APPLICANT: Gallichan, Scott
 APPLICANT: Lovitt, Corey
 APPLICANT: Parrington, Mark
 APPLICANT: Pedyczak, Artur
 APPLICANT: Radvanyi, Laszlo
 APPLICANT: Singh-Sandhu, Devender
 APPLICANT: Oomen, Raymond P

APPLICANT: Cao, Shi-Xian
 ; TITLE OF INVENTION: Tumor Antigens BFA4 and BCY1 for Prevention and/or Treatment of
 ; FILE REFERENCE: API-02-11-US
 ; CURRENT APPLICATION NUMBER: US/10/611,440

PRIOR FILING DATE: 2003-07-01
 PRIOR APPLICATION NUMBER: US 60/394,346
 PRIOR FILING DATE: 2002-07-03
 PRIOR APPLICATION NUMBER: US 60/394,503
 PRIOR FILING DATE: 2002-07-09
 PRIOR APPLICATION NUMBER: US 60/411,833
 PRIOR FILING DATE: 2002-09-18
 PRIOR APPLICATION NUMBER: US 60/445,342
 PRIOR FILING DATE: 2003-02-06
 NUMBER OF SEQ ID NOS: 218
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 188

LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: CLP-2825
 US-10-611-440-188

Query Match 44.9%; Score 31; DB 17; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.5e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPL 11
 Db 2 ETSPL 8

RESULT 11

US-10-437-708-168
 ; Sequence 168, Application US/10437708
 ; Publication No. US20040009555A1
 ; GENERAL INFORMATION:

APPLICANT: Kieleszewski, Marcia
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 ; FILE REFERENCE: OHU-04089
 ; CURRENT APPLICATION NUMBER: US/10/437,708
 ; CURRENT FILING DATE: 2003-05-14
 ; PRIOR APPLICATION NUMBER: US/09/547,693
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 236
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 168

LENGTH: 8

TYPE: PRT
 ; ORGANISM: Artificial/Unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Synthetic
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (3)..(4)
 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
 US-10-437-708-168

Query Match 43.5%; Score 30; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPL 10
 Db 1 PTPPL 5

RESULT 12

US-10-257-199-168
 ; Sequence 168, Application US/10257199
 ; Publication No. US20040230032A1
 ; GENERAL INFORMATION:

APPLICANT: Kieleszewski, Marcia
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 ; FILE REFERENCE: OHU-06319
 ; CURRENT APPLICATION NUMBER: US/10/257,199
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 09/547,693
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 244
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 168

LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (3)..(4)
 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
 US-10-257-199-168

Query Match 43.5%; Score 30; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPL 10
 Db 1 PTPPL 5

RESULT 13

US-10-190-082-480
 ; Sequence 480, Application US/10190082
 ; Publication No. US20030148264A1
 ; GENERAL INFORMATION:

APPLICANT: Laeky, Lawrence A.
 ; APPLICANT: Sidhu, Sandev S.
 ; APPLICANT: Held, Heike A.
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS


```

; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03/634
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 480
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-480

```

```

Query Match      43.5%; Score 30; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      6 PTPPLW 11
        |||||
Db      1 PNPFRW 6

```

```

RESULT 14
US-10-437-708-165
; Sequence 165, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-165

```

```

Query Match      43.5%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 PTPPL 10
        |||||
Db      3 PTPPL 7

```

```

RESULT 15
US-10-257-199-165
; Sequence 165, Application US/10257199
; Publication No. US20040230032A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-06319
; CURRENT APPLICATION NUMBER: US/10/257,199
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-257-199-165

```

```

Query Match      43.5%; Score 30; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 PTPPL 10
        |||||
Db      3 PTPPL 7

```

```

Search completed: January 6, 2005, 11:38:37
Job time : 141 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 11:18:11 ; Search time 38 Seconds
(without alignments)
20.943 Million cell updates/sec

Title: US-10-047-945-4
Perfect score: 69
Sequence: 1 LKMDPTPLMT 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A COMB pep:*
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3: /cgn2_6/ptodata/1/1aa/6A COMB pep:*
4: /cgn2_6/ptodata/1/1aa/6B COMB pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	78.3	10	1	US-08-657-163A-2
2	32	46.4	11	1	US-08-336-343A-31
3	32	46.4	11	3	US-08-652-877-31
4	32	46.4	11	3	US-08-476-515A-31
5	32	46.4	12	3	US-08-602-999A-252
6	32	46.4	12	3	US-09-500-124-252
7	30	43.5	6	3	US-09-232-446B-24
8	30	43.5	8	4	US-09-547-693-168
9	30	43.5	10	4	US-09-547-693-165
10	29	42.0	12	4	US-09-315-926A-18
11	28	40.6	10	3	US-09-133-341-7
12	28	40.6	10	4	US-09-739-852-7
13	27	39.1	6	1	US-07-989-290-2
14	27	39.1	6	1	US-08-271-698-2
15	27	39.1	6	1	US-08-468-596-2
16	27	39.1	6	4	US-09-295-996B-12
17	27	39.1	6	4	US-09-295-996B-15
18	27	39.1	6	4	US-09-551-737C-15
19	27	39.1	6	4	US-09-295-924B-2
20	27	39.1	6	4	US-09-551-738B-12
21	27	39.1	7	1	US-07-989-290-3
22	27	39.1	7	1	US-08-271-698-3
23	27	39.1	7	1	US-08-468-596-3
24	27	39.1	7	4	US-09-295-996B-13
25	27	39.1	7	4	US-09-295-996B-16
26	27	39.1	7	4	US-09-551-737C-16
27	27	39.1	7	4	US-09-295-924B-3

ALIGNMENTS

28	27	39.1	7	4	US-09-551-738B-13	Sequence 13, Appl
29	27	39.1	8	1	US-07-989-290-4	Sequence 4, Appl
30	27	39.1	8	1	US-08-271-698-4	Sequence 4, Appl
31	27	39.1	8	1	US-08-468-596-4	Sequence 4, Appl
32	27	39.1	8	4	US-09-295-996B-14	Sequence 14, Appl
33	27	39.1	8	4	US-09-295-996B-17	Sequence 17, Appl
34	27	39.1	8	4	US-09-551-737C-17	Sequence 17, Appl
35	27	39.1	8	4	US-09-295-924B-4	Sequence 14, Appl
36	27	39.1	8	4	US-09-551-738B-14	Sequence 14, Appl
37	27	39.1	10	4	US-09-295-996B-8	Sequence 11, Appl
38	27	39.1	10	4	US-09-295-996B-11	Sequence 11, Appl
39	27	39.1	10	4	US-09-551-737C-11	Sequence 7, Appl
40	27	39.1	10	4	US-09-295-924B-7	Sequence 7, Appl
41	27	39.1	10	4	US-09-551-738B-8	Sequence 8, Appl
42	27	39.1	11	1	US-09-393-941-3	Sequence 3, Appl
43	27	39.1	11	1	US-08-175-471-3	Sequence 3, Appl
44	27	39.1	11	2	US-08-429-054A-3	Sequence 3, Appl
45	27	39.1	11	2	US-08-718-777-3	Sequence 3, Appl

RESULT 1
US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LIPNS AND THEIR
UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULAR TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N

STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
STREET: 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
US-08-476-515A-31

Query Match 46.4%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KANDPTPL 10
Db 3 KMPMPRPL 11

RESULT 5
US-08-602-999A-252
Sequence 252, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-252

Query Match 46.4%; Score 32; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KANDPTPL 10
Db 4 KMPMPRPL 12

RESULT 6
US-09-500-124-252
Sequence 252, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEFAX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-09-500-124-252

Query Match 46.4%; Score 32; DB 4; Length 12;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMPPTPL 10
 Db 4 KMPPTPL 12

RESULT 7
 US-09-232-446B-24
 Sequence 24, Application US/09232446B
 Patent No. 6228647
 GENERAL INFORMATION:
 APPLICANT: Voytas, Daniel F.
 TITLE OF INVENTION: Transposable Element Protein that Directs DNA
 FILE OF INVENTION: Integration to Specific Chromosomal Sites
 FILE REFERENCE: 2-98
 CURRENT APPLICATION NUMBER: US/09/232,446B
 PRIOR FILING DATE: 1999-01-15
 PRIOR APPLICATION NUMBER: US 60/071,383
 PRIOR FILING DATE: 1998-01-15
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 24
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
 OTHER INFORMATION: sequence
 US-09-232-446B-24

Query Match 43.5%; Score 30; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTTP 9
 Db 1 LDPTSP 6

RESULT 8
 US-09-547-693-168
 Sequence 168, Application US/09547693
 Patent No. 6639050
 GENERAL INFORMATION:
 APPLICANT: Kleiszewski, Marcia
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 FILE OF INVENTION: Glycoproteins
 FILE REFERENCE: OHU-04089
 CURRENT APPLICATION NUMBER: US/09/547,693
 PRIOR FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 236
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 168
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: misc_feature

OTHER INFORMATION: Synthetic
 NAME/KEY: SITE
 LOCATION: (1)..(1)
 OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 NAME/KEY: SITE
 LOCATION: (3)..(4)
 OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
 US-09-547-693-168

Query Match 43.5%; Score 30; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPL 10
 Db 1 PTPL 5

RESULT 9
 US-09-547-693-165
 Sequence 165, Application US/09547693
 Patent No. 6639050
 GENERAL INFORMATION:
 APPLICANT: Kleiszewski, Marcia
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 FILE OF INVENTION: Glycoproteins
 FILE REFERENCE: OHU-04089
 CURRENT APPLICATION NUMBER: US/09/547,693
 PRIOR FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 236
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 165
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial/Unknown
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Synthetic
 NAME/KEY: SITE
 LOCATION: (1)..(1)
 OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 NAME/KEY: SITE
 LOCATION: (3)..(3)
 OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 NAME/KEY: SITE
 LOCATION: (5)..(6)
 OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
 US-09-547-693-165

Query Match 43.5%; Score 30; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPL 10
 Db 3 PTPL 7

RESULT 10
 US-09-315-926A-18
 Sequence 18, Application US/09315926A
 Patent No. 6498027
 GENERAL INFORMATION:
 APPLICANT: Es van, Helmut
 APPLICANT: Havenga, Menno
 APPLICANT: Verlinden, Stefan
 TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
 FILE REFERENCE: 2183-4080US
 CURRENT APPLICATION NUMBER: US/09/315,926A
 PRIOR FILING DATE: 1999-05-20
 CURRENT APPLICATION NUMBER: EP 99201593.3
 PRIOR FILING DATE: 1999-05-20
 PRIOR APPLICATION NUMBER: EP 99201693.3

PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: phage display peptide
US-09-315-926A-18

Query Match 42.0%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPTPLW 11
DB 7 TPTPLW 11

RESULT 11
US-09-133-341-7
Sequence 7, Application US/09133341A
Patent No. 6162440
GENERAL INFORMATION:
APPLICANT: Hayward, Diane S.
APPLICANT: Ling, Paul D.
TITLE OF INVENTION: EBN2 PEPTIDES AND METHODS OF USING SAME
FILE REFERENCE: 87512
CURRENT APPLICATION NUMBER: US/09/133,341A
CURRENT FILING DATE: 1998-08-13
EARLIER APPLICATION NUMBER: WO 97US2243
EARLIER FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 10
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Virus Organism: Artificial
US-09-133-341-7

Query Match 40.6%; Score 28; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TPTPLW 11
DB 2 PGPPPW 7

RESULT 12
US-09-739-852-7
Sequence 7, Application US/09739852
Patent No. 6495144
GENERAL INFORMATION:
APPLICANT: Hayward, Diane S.
APPLICANT: Ling, Paul D.
TITLE OF INVENTION: EBN2 PEPTIDES AND METHODS OF USING SAME
FILE REFERENCE: 87512
CURRENT APPLICATION NUMBER: US/09/739,852
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 09/133,341
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 10
TYPE: PRT
ORGANISM: Unknown
FEATURE:

OTHER INFORMATION: Description of Unknown Virus Organism: Artificial
US-09-739-852-7

Query Match 40.6%; Score 28; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TPTPLW 11
DB 2 PGPPPW 7

RESULT 13
US-07-989-290-2
Sequence 2, Application US/07989290
Patent No. 5358934
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP/S&S-127
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-989-290-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
DB 2 DPAPP 6

RESULT 14
US-08-271-698-2
Sequence 2, Application US/08271698
Patent No. 5439821
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Peats
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-271-698-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

RESULT 15
US-08-468-596-2
Sequence 2, Application US/08468596
Patent No. 5629196
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Peats
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,698
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-596-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 2 DPAPP 6

Search completed: January 6, 2005, 11:27:54
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:21 ; Search time 15.6757 Seconds
(without alignments)
61.380 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMDPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	77.8	398	2	A81717	conserved hypothet
2	38	70.4	792	2	T29187	hypothetical prote
3	38	70.4	1325	2	S62497	probable nucleopor
4	37	68.5	142	2	A81681	similar o transcri
5	37	68.5	212	2	C87585	hypothetical prote
6	37	68.5	237	2	A42013	alpha-1-B-glycopro
7	37	68.5	286	2	S72384	hypothetical prote
8	37	68.5	429	2	S09852	hypothetical prote
9	37	68.5	450	2	B47265	tailless (C11) pro
10	37	68.5	452	2	A35602	tailless (C11) pro
11	37	68.5	1819	2	T32008	hypothetical prote
12	36	66.7	117	2	AF3319	hypothetical prote
13	36	66.7	222	2	C71955	hypothetical prote
14	36	66.7	365	2	F87552	cdpr4 protein (limp
15	36	66.7	392	2	T29519	hypothetical prote
16	36	66.7	431	2	T29716	hypothetical prote
17	36	66.7	460	2	H70986	probable hydroxylas
18	36	66.7	480	2	T49096	hypothetical prote
19	36	66.7	898	2	T21179	hypothetical prote
20	36	66.7	944	2	A89624	protein F2A10.2 l
21	36	66.7	968	2	T46568	ATP-dependent RNA
22	36	66.7	2717	2	A34203	DNAB-binding protei
23	35	64.8	159	2	S61040	probable membrane
24	35	64.8	206	2	S50913	TAR25 protein - ye
25	35	64.8	262	2	B64679	tryptophan synthas
26	35	64.8	291	2	AH2017	lipotic acid synthet
27	35	64.8	313	2	A95859	conserved hypothet
28	35	64.8	323	1	TVMTF6	protein kinase (EC
29	35	64.8	380	1	TVFTMM	protein kinase (EC

30	35	64.8	382	1	TVBE61	protein kinase (EC
31	35	64.8	382	1	TVBE6A	protein kinase (EC
32	35	64.8	384	2	T42612	probable protein k
33	35	64.8	543	2	A53790	cytochrome P450-EP
34	35	64.8	587	2	I40849	succinate dehydrog
35	35	64.8	602	1	TVRTRR	protein kinase (EC
36	35	64.8	627	2	T18772	hypothetical prote
37	35	64.8	647	1	S00644	protein kinase raf
38	35	64.8	648	1	TVRDF6	protein kinase raf
39	35	64.8	648	1	TVRTRF	protein kinase raf
40	35	64.8	648	2	A25047	beta-glucuronidase
41	35	64.8	657	2	A53545	protein p84 - huma
42	35	64.8	678	2	T50256	probable vacuolar
43	35	64.8	765	2	T35719	chitinase - Strept
44	35	64.8	825	1	EDBEKD	chitinase-early pr
45	35	64.8	1397	2	T46354	hypothetical prote

ALIGNMENTS

RESULT 1
A81717
conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain N199)
C:Species: Chlamydia muridarum, Chlamydia trachomatis McPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #ext_change 09-Jul-2004
C:Accession: A81717
R:Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salberg
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis McPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MID:20150255; PMID:10684935
A:Accession: A81717
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <TEXT>
A:Cross-references: UNIPROT:O9PL02; GB:AE002298; GB:AE002160; NID:G7190343; PIDN:AAF391.
A:Experimental source: strain N199 (Mcpn)
C:Gene: TC0306
C:Superfamily: Chlamydia trachomatis hypothetical protein CT036

Query Match 77.8%; Score 42; DB 2; Length 398;
Best Local Similarity 77.8%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
| : |||||
Db 309 KELDPTPL 317

RESULT 2
T29187
hypothetical protein C55C3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
C:Accession: T29187
R:Woesne, J.; Steillyes, L.
Submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C55C3.
A:Reference number: Z20585
A:Accession: T29187
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-792 <WOE>
A:Cross-references: EMBL:U53335; PIDN:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3
A:Experimental source: strain Bristol N2; clone C55C3
C:Gene: C55C3.3
A:Map position: 4
A:Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 4

Query Match 70.4%; Score 38; DB 2; Length 792;

Best Local Similarity 87.5%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
Db 133 LKAMDPTP 140

RESULT 3

S62497
probable nucleoporin - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62497; T38281
R:Niblett, D.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62492
A:Accession: S62497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1325 <NIB>
A:Cross-references: UNIPROT:Q09847; EMBL:Z64354; NID:g1039338; PIDN:CAA91241.1; PID:g103
R:Niblett, D.; Harris, D.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21783
A:Accession: T38281
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1325 <NIB>
A:Cross-references: EMBL:Z64354; PIDN:CAA91241.1; GSPDB:GNO0066; SPDB:SPAC33D3.06c
A:Experimental source: strain 972h-; cosmid c23D3
C:Genetics:
A:Gene: SPAC33D3.06c
A:Map position: 1R
A:introns: 33/3

Query Match 70.4%; Score 38; DB 2; Length 1325;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 KAMDPTP 9
Db 299 KAMDPTP 306

RESULT 4

AB1681
similar o transcription regulators lin1991 [imported] - Listeria innocua (strain Clp112
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1681
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fath, H.
Science 294, 849-852, 2001
A:Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tlertaz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1681
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <GIA>
A:Cross-references: UNIPROT:Q092AD1; GB:AL592022; PIDN:CAC97221.1; PID:g16414492; GSPDB:G
C:Genetics:
A:Genes: lin1991
A:Superfamily: conserved hypothetical protein M0568

Query Match 68.5%; Score 37; DB 2; Length 142;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTP 9
Db 130 LKAMDPTP 138

RESULT 5

C87585
hypothetical protein CC2714 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87585
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Ijamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Brmoleva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frazer, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87585
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <STO>
A:Cross-references: UNIPROT:Q2A4M1; GB:AE005673; NID:g13424303; PIDN:AAK24679.1; GSPDB:G
C:Genetics:
A:Gene: CC2714

Query Match 68.5%; Score 37; DB 2; Length 212;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 KAMDPTP 9
Db 52 RSLDPTP 59

RESULT 6

A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42013
R:Caranese, J.J.; Kreng, L.F.
Biochemistry 31, 410-418, 1992
A:Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum
A:Reference number: A42013; MUID:92118834; PMID:1731898
A:Accession: A42013
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-237 <CAT>
A:Cross-references: UNIPROT:Q28359; GB:U05356
C:Keywords: glycoprotein

Query Match 68.5%; Score 37; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LKAMDPTP 10
Db 1 LKAMDPTP 10

RESULT 7

S72384
hypothetical protein 8 precursor - Enterococcus faecalis plasmid pAD1
C:Species: Enterococcus faecalis
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S72384
R:Hirt, H.; Wirth, R.; Muscholl, A.
Mol. Gen. Genet. 252, 640-647, 1996
A:Title: Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: d
A:Reference number: S72375; MUID:97074879; PMID:8917306
A:Accession: S72384
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-286 <HIR>
 A:Cross-references: UNIPROT:Q47791; EMBL:X96977; NID:91279406; PIDN:CAA65667.1; PID:9127
 A:Experimental source: strain OGIX
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Genome: plasmid PAD1
 C:Superfamily: probable pheromone-responsive protein
 F1-26/Domain: signal sequence #status predicted <SIG>
 F1-27-286/Product: hypothetical protein 8 #status predicted <MAT>

Query Match 68.5%; Score 37; DB 2; Length 286;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
 DB 50 KPTDPTPPI 58

RESULT 8
 509852
 Hypothetical protein UN88 - human cytomegalovirus (strain AD169)
 C:Species: human cytomegalovirus, human herpesvirus 5
 A:Note: host Homo sapiens (man)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: 509852
 R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohm, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
 M.; Barrett, B.G.
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
 A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
 A:Reference number: S09749; MID:90269039; PMID:2161139
 A:Accession: S09852
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-429 <CHB>
 A:Cross-references: UNIPROT:P16731; EMBL:X17403; NID:959591; PIDN:CAA35362.1; PID:917808
 A:Note: this sequence was submitted to the EMBL Data Library, December 1989

Query Match 68.5%; Score 37; DB 2; Length 429;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
 DB 348 LKALDPPPP 356

RESULT 9
 B47265
 tailless (tll) protein - fruit fly (Drosophila virilis)
 C:Species: Drosophila virilis
 C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
 C:Accession: B47265
 R:Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
 A:Title: Characterization of downstream elements in a Raf-1 pathway.
 A:Reference number: A47265; MID:93157371; PMID:8430097
 A:Accession: B47265
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <LTA>
 A:Cross-references: GBL:104955
 C:Genetics:
 A:Gene: FlyBase:FlyBase:DV1r/tll
 A:Cross-references: FlyBase:FlyBase:FBgn0013145
 C:Superfamily: erba transforming protein homology
 C:Keywords: zinc finger
 F1-32-339/Domain: erba transforming protein homology <ERBA>

Query Match 68.5%; Score 37; DB 2; Length 450;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
 DB 216 RALPPTPPL 224

RESULT 10
 A35602
 tailless (tll) protein - fruit fly (Drosophila melanogaster)
 N:Alternate names: steroid hormone receptor homolog tll; transcription factor tll
 C:Species: Drosophila melanogaster
 C>Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 C:Accession: A35602
 R:Pignoni, F.; Balderelli, R.M.; Steingrimsson, E.; Diaz, R.J.; Patapoutian, A.; Merriam
 Cell 62, 151-163, 1990
 A:Title: The Drosophila gene tailless is expressed at the embryonic termini and is a me
 A:Reference number: A35602; MID:90304905; PMID:2364433
 A:Accession: A35602
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <PIG>
 A:Cross-references: UNIPROT:P18102; GB:X52147
 R:Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
 A:Title: Characterization of downstream elements in a Raf-1 pathway.
 A:Reference number: A47265; MID:93157371; PMID:8430097
 A:Accession: A47265
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-452 <LTA>
 A:Cross-references: GBL:AF019362; GBL:104954; NID:92429340; PIDN:AA871371.1; PID:92440022
 A:Note: sequence extracted from NCBI backbone (NCBIN:124057, NCBI:124058)
 C:Genetics:
 A:Gene: tll
 A:Cross-references: FlyBase:FBgn003720
 A:Note: tailless
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc finger.
 F1-32-341/Domain: erba transforming protein homology <ERBA>

Query Match 68.5%; Score 37; DB 2; Length 452;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
 DB 218 RALPPTPPL 226

RESULT 11
 T32008
 hypothetical protein K10G6.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32008
 R:Davidson, S.; Wohldmann, P.; Mullen, G.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid K10G6.
 A:Reference number: Z21111
 A:Accession: T32008
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1819 <DAV>
 A:Cross-references: UNIPROT:O16625; EMBL:AF016669; PIDN:AA866098.1; GSPDB:GNO0020; CESP
 A:Experimental source: strain Bristol N2; Clone K10G6
 C:Genetics:
 A:Gene: CESP:K10G6.3
 A:Map position: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
 A:introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query Match 68.5%; Score 37; DB 2; Length 1819;
 Best Local Similarity 66.7%; Pred. No. 3,6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMPDPRP 9
|:|||||
Db 500 LKMTDPRP 508

RESULT 12

AF3319
hypotheetical protein BME10540 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AF3319
R:Belvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,
.; Mazur, M.; Goldsman, B.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3319
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KUR>
A:Cross-references: UNIPROT:Q8YIA5; GB:AE008917; PIDN:AAL51721.1; PID:gt7982457; GSPDB:C
C:Genetics:
A:Gene: BME10540
A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 KAMPDPRP 10
|:|||||
Db 83 KACDPLPMP 91

RESULT 13
C71955
hypotheetical protein jhp0241 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: C71955
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R.;
.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: C71955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <ARN>
A:Cross-references: UNIPROT:Q9ZMH9; GB:AB001462; GB:AB001439; NID:g4154760; PIDN:AAD0583
C:Genetics:
A:Experimental source: strain J99
A:Gene: jhp0241

Query Match 66.7%; Score 36; DB 2; Length 222;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 KAMPDPRP 9
|:|||||
Db 193 KTTDPRP 200

RESULT 14
P87552
dprA protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: P87552
R:Netman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: P87552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q9A5K0; GB:AE05673; NID:g1342392; PIDN:AAK24418.1; GSPDB:G
C:Genetics:
A:Gene: CC2447

Query Match

66.7%; Score 36; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMPDPRP 10
|:|||||
Db 92 LKAMPDPRP 101

RESULT 15

T29519
hypotheetical protein T29510.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29519
R:Pauley, A.; Gattung, S.
Submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid T29510.
A:Reference number: Z20634
A:Accession: T29519
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <PAU>
A:Cross-references: UNIPROT:Q23048; EMBL:U64856; PIDN:AAE04987.1; GSPDB:GN00023; CESP:T2
A:Experimental source: strain Bristol N2; clone T29510
C:Genetics:
A:Gene: CESP:T29510.4
A:Map position: 5
A:introns: 38/3; 84/2; 156/3; 182/3; 228/3; 256/1; 312/2; 337/3; 361/2

Query Match 66.7%; Score 36; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPPL 10
|:|||||
Db 291 DPTPPL 296

Search completed: January 6, 2005, 10:23:46
Job time : 17.6757 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2005, 10:00:35 ; Search time 85.6757 Seconds
(without alignments)
67.157 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	17	Q9TR78	Q9TR78 didelphis m
2	54	100.0	291	DM43_DIDMR	P82957 didelphis m
3	45	83.3	140	Q8H275	Q8H275 didelphis m
4	45	83.3	291	Q8H274	Q8H274 didelphis m
5	42	77.8	398	Y306_CHLMU	Q9P102 chlamydia m
6	41	75.9	99	Q6CS47	Q6CS47 kluyveromyc
7	41	75.9	165	Q9W3H5	Q9W3H5 drosoephila
8	39	72.2	98	Q853J7	Q853J7 mycobacteri
9	39	72.2	156	Q8MLX6	Q8MLX6 echinococcu
10	39	72.2	227	Q73ZB2	Q73ZB2 mycobacteri
11	39	72.2	237	AA504008	AA504008 mycobacte
12	39	72.2	243	Q961D3	Q961D3 homo sapien
13	39	72.2	268	Q6G1P6	Q6G1P6 bartonella
14	39	72.2	320	Q8V3M1	Q8V3M1 swinepox vi
15	39	72.2	633	Q9K437	Q9K437 streptomyce
16	39	72.2	754	KB15_HUMAN	KB15_HUMAN
17	39	72.2	829	AAH02799	AAH02799 homo sapi
18	39	72.2	849	Q6NV16	Q6NV16 homo sapien
19	39	72.2	849	AAH68014	AAH68014 homo sapi
20	38	70.4	86	Q6FV03	Q6FV03 candida gla
21	38	70.4	274	Q95006	Q95006 caenorhabdi
22	38	70.4	302	Q8CBA3	Q8CBA3 mus musculu
23	38	70.4	369	Q42606	Q42606 arabidopsis
24	38	70.4	369	Q96532	Q96532 arabidopsis
25	38	70.4	560	Q6C7D9	Q6C7D9 yarrowia ii
26	38	70.4	881	Q9NE42	Q9NE42 leishmania
27	38	70.4	1325	YAB6_SCHPO	YAB6_SCHPO
28	38	70.4	1345	Q8C1P5	Q8C1P5 mus musculu
29	37	68.5	70	Q7PIK7	Q7PIK7 anopheles g
30	37	68.5	107	Q36604	Q36604 hepatitis e
31	37	68.5	142	MATR_LISIN	Q92ad1 listeria in

32	37	68.5	156	2	Q8WPI6	Q8WPI6 echinococcu
33	37	68.5	212	2	Q9A4W1	Q9A4W1 cauliobacter
34	37	68.5	242	2	Q8BXK6	Q8BXK6 mus musculu
35	37	68.5	270	2	Q8KUD2	Q8KUD2 enterococcu
36	37	68.5	271	2	Q838G9	Q838G9 enterococcu
37	37	68.5	286	2	Q47791	Q47791 enterococcu
38	37	68.5	286	2	Q9F1F9	Q9F1F9 enterococcu
39	37	68.5	286	2	Q82Y86	Q82Y86 enterococcu
40	37	68.5	314	2	Q8H7X5	Q8H7X5 didelphis m
41	37	68.5	316	2	Q6NAY5	Q6NAY5 rhodopsinu
42	37	68.5	316	2	CAE26488	CAE26488 rhodopsu
43	37	68.5	393	2	Q70J80	Q70J80 streptomyce
44	37	68.5	393	2	CAR17535	CAR17535 streptomy
45	37	68.5	429	1	UL68_HCMVA	P16731 human cytom

ALIGNMENTS

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RESULT 1
Q9TR78      PRELIMINARY;      PRT;      17 AA.
ID   Q9TR78
AC   Q9TR78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE   ANTI-BOTROPIC complex 48,000 SUBUNIT (Fragment).
OC   Didelphis marsupialis (Southern opossum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX   NCBI_TaxID=9268;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95149299; PubMed=7846694;
RA   Perales J., Moussette H., Marangoni S., Oliveira B., Domont G.B.;
RT   "Isolation and partial characterization of an anti-botropic complex
RT   from the serum of South American Didelphidae.";
RL   Toxicon 32:1237-1249(1994).
SQ   SEQUENCE   17 AA;  1947 MW;  CBS5FB40E73B2A2A CRC64;

Query Match      100.0%; Score 54; DB 2; Length 17;
Best local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMPPTPL 10
Db      1 LKAMPPTPL 10

RESULT 2
DM43_DIDMR      STANDARD;      PRT;      291 AA.
ID   DM43_DIDMR
AC   P82957;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Venom metalloproteinase inhibitor DM43.
OC   Didelphis marsupialis (Southern opossum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX   NCBI_TaxID=9268;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Serum;
RX   MEDLINE=21953368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA   Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.;
RA   Makino D.L., Garratt R.C., Domont G.B.;
RT   "Structural and functional analyses of DM43, a snake venom
RT   metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL   J. Biol. Chem. 277:13129-13137(2002).
CC   -1- FUNCTION: Metalloproteinase inhibitor.
CC   -1- SUBUNIT: Homodimer.
CC   -1- TISSUE SPECIFICITY: Blood and milk.

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CC -1- P1M: N-glycosylated.
CC -1- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011015; IEM-like.
DR Pfam: PF00047; IG_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KM Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79 IG-like V-type 1.
FT DOMAIN 114 171 IG-like V-type 2.
FT DOMAIN 191 288 IG-like V-type 3.
FT DISULFID 28 74 Potential.
FT DISULFID 121 163
FT DISULFID 213 265
FT CARBOHYD 23 23 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 291 AA; 32390 MW; 17A496227B69A65B CRC64;

Query Match 100.0%; Score 54; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LKAMDPTPPL 10
DB 1 LKAMDPTPPL 10

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RESULT 3
Q8H275 PRELIMINARY; PRT; 140 AA.
AC Q8H275;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP51-D (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN 1
RP SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131000; AAN06911.1; -.
DR InterPro: IPR011015; IEM-like.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

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Query Match 83.3%; Score 45; DB 2; Length 140;
Best Local Similarity 90.0%; Pred. No. 7.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LKAMDPTPPL 10
DB 42 LKAMDPTPRL 51

RESULT 4
Q8H274 PRELIMINARY; PRT; 291 AA.
AC Q8H274;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP14 (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

```

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OX NCBI_TaxID=9267;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131001; AAN06912.1; -.
DR InterPro: IPR003599; IG_1.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011015; IEM-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 291
SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0B84 CRC64;

Query Match 83.3%; Score 45; DB 2; Length 291;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LKAMDPTPPL 10
DB 1 LKAMDPTPRL 10

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RESULT 5
Y306_CHLMU STANDARD; PRT; 398 AA.
ID Y306_CHLMU
AC Q9PL02;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TC0306.
GN OrderedLocustNames=TC0306;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=MOPn / N199;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Ullrichback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Nelson M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the chlamydial Cpn0129/Cr036/TC0306 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE002298; AAF39171.1; -.
DR PIR; A81717; A81717.
DR TIGR; TC0306; -.
KM Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 31 51 Potential.
FT TRANSMEM 56 76 Potential.
SQ SEQUENCE 398 AA; 44639 MW; 8CD8E541C5C92A88 CRC64;

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Query Match 77.8%; Score 42; DB 1; Length 398;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 KAMDPPTPL 10
|:|||||
Db 309 KAMDPTPL 317

RESULT 6
Q6CS47
ID Q6CS47 PRELIMINARY; PRT; 99 AA.
AC Q6CS47
DT 01-OCT-2004 (TEMBLrel. 28, Created)
DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
DE 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
DB Similar to sgdlS0007245 Saccharomyces cerevisiae YKL016ca COX19.
GN ORFNames=K1LA00039719;
OS Kluveromyces laetis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG GENOME/VRRES;
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla B., Barbe V.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
RA Boissame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre J., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerest J.M., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.M., Mikolaj M., Ozras S., Ozier-Kalogeropoulos O.,
RA Bellanz S., Pocher S., Richard G.F., Straub M.L., Suleau A.,
RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Weyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL:CR382124; CAH00338.1; -; 032BA5D3C50CAC2 CRC64;
SQ SEQUENCE 99 AA; 11050 MW; 032BA5D3C50CAC2 CRC64;

Query Match 75.3%; Score 41; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 9
|:|||||
Db 9 LKALSTPL 17

RESULT 7
Q9W3H5
ID Q9W3H5 PRELIMINARY; PRT; 165 AA.
AC Q9W3H5
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DN CG2147-PA (LP02728p).
GN ORFNames=CG2147;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RX Adame M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Abpayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke J., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheieler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Zibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Ceiniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=22426069; PubMed=12537572;
RX Mista S., Crosby M.A., Mungall C.U., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochkin S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.

```

RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
  Champs M., Chavez C., Dorsett V., Dreanek D., Fattan D., Frise E.,
  George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liso G.,
  Miranda A., Mungall C.J., Nuno J., Pacle J., Paragas V., Park S.,
  Patel S., Pounanavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
  Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003443; AA046352.1; -
DR EMBL; AY069722; AA039867.1; -
DR Intact; Q9W3H5; -
DR FLYBASE; FBgn0030025; CG2147.
SQ SEQUENCE 165 AA; 17157 MW; CR3BD2E102302C2 CRC64;

Query Match          75.9%; Score 41; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPPL 10
   |||||
Db 1 MDPTPPL 7

RESULT 8
Q853J7 PRELIMINARY; PRT; 98 AA.
AC Q853J7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp80.
OS Mycobacteriophage Bx21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22592660; PubMed=12705866;
RA Pedula M.L., Ford M.E., Houz J.M., Karthikeyan T., Wadsworth C.,
  Lewis J.A., Jacobs-Sera D., Palbo J., Gross J., Pannunzio N.R.,
  Brucker W., Kumar V., Kandassamy J., Keenan L., Bardarov S.,
  Krizkov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
  Hatfull G.F.;
RL "Origins of highly mosaic mycobacteriophage genomes.",
  Cell 113:171-182(2003).
DR EMBL; AY129337; AA016740.1; -
SQ SEQUENCE 98 AA; 10867 MW; D1D8F87C4CD15B CRC64;

Query Match          72.2%; Score 39; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAMDPTPP 9
   |||||
Db 29 QALDPTPP 36

RESULT 9
Q8MLX6 PRELIMINARY; PRT; 156 AA.
AC Q8MLX6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE EM95 vaccine antigen.
OS Eschinococcus multilocularis.

```

```

OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Echinococcus.
OX NCBI_TaxID=6211;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22060722; PubMed=12065546;
RA Gauci C., Merli M., Muller V., Chow C., Yagi K., Mackenstedt U.,
  Lightowler M.W.;
RL "Molecular cloning of a vaccine antigen against infection with the
  larval stage of Echinococcus multilocularis.",
  Infect. Immun. 70:3969-3972(2002).
DR EMBL; AY062920; AA051152.1; -
DR EMBL; AY062921; AA051153.1; -
DR InterPro; IPR003961; FN.II.
DR InterPro; IPR008957; FN.III-1like.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS00853; FN3; 1.
SQ SEQUENCE 156 AA; 17145 MW; P96B940A0D5B731D CRC64;

Query Match          72.2%; Score 39; DB 2; Length 156;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
   |||||
Db 66 LKALDPSDPL 75

RESULT 10
Q73ZB2 PRELIMINARY; PRT; 227 AA.
AC Q73ZB2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MAP1691c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X10;
RA Li L., Bannantine J., Zhang O., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017233; AA004008.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0EB199 CRC64;

Query Match          72.2%; Score 39; DB 2; Length 227;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
   |||||
Db 146 LKALDPTPPL 155

RESULT 11
AA004008 PRELIMINARY; PRT; 227 AA.
AC AA004008;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN MAP1691C.
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OX NCBI_TaxID=1770;

```


RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; A501723; AAS04008.1; -
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962CEBE199 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 227;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 10
DB 146 LKAMDPTPP 155

RESULT 12

ID 0961D3 PRELIMINARY; PRT; 243 AA.
AC 0961D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE KIAA1115 protein (Fragment).
GN KIAA1115;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helen F.,
RA Dlatchenko L., Marusha K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarale P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyvinski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007629; AAH07629.1; -
FT NON TER 1 1
SQ SEQUENCE 243 AA; 24559 MW; 9094604DEA93228 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 243;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
DB 130 LKAMDPTPP 138

RESULT 13

ID 06G1P6 PRELIMINARY; PRT; 268 AA.
AC 06G1P6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.
GN Name=Plac; OrderedLocNames=BH16290;
OC Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_Taxid=38323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978;

RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canback B., Eriksson A.-S., Naslund A.K., Handley S.A., Huvel M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF28391.1; -
DR InterPro: IPR002123; Acyltransferase.
DR Pfam: PF01553; Acyltransferase; 1.
DR SMART; SM00563; Plac; 1.
KW Acyltransferase; Complete proteome; Transferase.
SQ SEQUENCE 268 AA; 30957 MW; 2F955B7EEFBD8B95 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 268;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
DB 240 LKAMDPTPP 248

RESULT 14

ID 08V3M1 PRELIMINARY; PRT; 320 AA.
AC 08V3M1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPV074 DNA topoisomerase.
GN Name=SPV074;
OS Swinepox virus (SWPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirub.

OC NCBI_Taxid=10276;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21624277; PubMed=11752168;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
RA Kutish G.F., Rock D.L.;
RT "The genome of swinepox virus.";
RL J. Virol. 76:783-790(2002).
DR EMBL; AF410153; AAL69813.1; -
DR HSSP; P08585; 1VCC.
DR GO; GO:0003677; rDNA binding; IEA.
DR GO; GO:000317; rDNA topoisomerase type I activity; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR GO; GO:0006268; P:DNA unwinding; IEA.
DR InterPro: IPR011010; DNA birk join enz.
DR InterPro: IPR001631; Topoisomerase I.
DR Pfam: PF01028; Topoisom I; 1.
DR PRINTS; PR00416; EUTPISMRAS1.
DR PROSITE; PS00176; TOPOISOMERASE_I_EUK; UNKNOWN_1.
KW Isomerase.
SQ SEQUENCE 320 AA; 38179 MW; 97F9B94442DD1DC5 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 320;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
 : : : : :
 DB 241 IKSLDPVPP 250

RESULT 15

09K437 PRELIMINARY; PRT; 693 AA.
 AC 09K437;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Putative hydrolase.
 GN OrderedLocustNames=SCO1062; ORFNames=SCG22.08c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.R., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch B., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939107; CAB95281.1; -
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR006101; Glyco_hydro_2.
 DR InterPro; IPR006102; Glyco_hydro_2ig.
 DR InterPro; IPR006104; Glyco_hydro_2SB.
 DR InterPro; IPR006103; Glyco_hydro_2TM.
 DR InterPro; IPR002088; PPTA.
 DR Pfam; PF00703; Glyco_hydro_2; 1.
 DR Pfam; PF02836; Glyco_hydro_2_C; 1.
 DR Pfam; PF02837; Glyco_hydro_2_N; 1.
 DR PRINTS; PR00132; GLHYDRLASE2.
 DR PROSITE; PS00904; PPTA; UNKNOWN_1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 693 AA; 75941 MW; E54676BCCA33A921 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 693;
 Best Local Similarity 70.0%; Pred. No. 4.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
 : : : : :
 DB 420 LKALDPTRPV 429

Search completed: January 6, 2005, 10:17:43
 Job time : 90.6757 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:08:37 ; Search time 79.4595 Seconds
(without alignments)
45.146 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPTPPL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 35872929 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Genesegp23sep04:*
2: genesegp19908:*
3: genesegp20008:*
4: genesegp20018:*
5: genesegp20028:*
6: genesegp20038:*
7: genesegp20038:*
8: genesegp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	100.0	10	2	AAW53843	AAW53843 N-terminu
2	54	100.0	10	7	ABB80222	Abb80222 Synthetic
3	54	100.0	11	7	ABB80226	Abb80226 Synthetic
4	54	100.0	12	7	ABB80225	Abb80225 Synthetic
5	54	100.0	15	2	AAW11575	AAW11575 N-terminu
6	54	100.0	15	2	AAW53841	AAW53841 N-terminu
7	54	100.0	15	7	ABB80223	Abb80223 Synthetic
8	50	92.6	9	7	ABB80227	Abb80227 Synthetic
9	43	79.6	8	7	ABB80228	Abb80228 Synthetic
10	42	77.8	94	4	AAO02179	AAO02179 Human pol
11	41	75.9	165	4	ABB58900	Abb58900 Drosophila
12	39	72.2	459	3	AAW59012	AAW59012 Breast an
13	38	70.4	78	4	AAW65892	AAW65892 Human imm
14	38	70.4	108	2	ABW74107	ABW74107 DNA clone
15	38	70.4	267	2	AAW43943	AAW43943 Yeast pro
16	38	70.4	349	3	AAW17097	AAW17097 Arabidops
17	38	70.4	369	3	AAW47069	AAW47069 Arabidops
18	38	70.4	369	3	AAW42323	AAW42323 Arabidops
19	38	70.4	369	5	AAW93666	AAW93666 Herbicide
20	38	70.4	405	3	AAW47028	AAW47028 Arabidops
21	37	68.5	15	2	AAW39043	AAW39043 Peptide r
22	37	68.5	210	5	AAW00125	AAW00125 Enterococ
23	37	68.5	210	5	ABP43344	ABP43344 B faecali
24	37	68.5	210	6	ABU88372	ABU88372 B. faecal
25	37	68.5	210	6	ABU13623	ABU13623 Enterococ

ALIGNMENTS

26	37	68.5	256	2	AAW00124	AAW00124 Enterococ
27	37	68.5	256	5	ABP43343	ABP43343 B faecali
28	37	68.5	256	6	ABU88371	ABU88371 B. faecal
29	37	68.5	256	6	ABU13622	ABU13622 Enterococ
30	37	68.5	270	6	ABU29194	ABU29194 Protein e
31	37	68.5	285	6	ABU28946	ABU28946 Protein e
32	37	68.5	291	7	ADH88791	ADH88791 Enterococ
33	37	68.5	306	7	ADH88698	ADH88698 Enterococ
34	37	68.5	452	4	ABB58056	ABB58056 Drosophila
35	36	66.7	86	4	ABG17160	ABG17160 Novel hum
36	36	66.7	86	7	ADP60462	ADP60462 Human con
37	36	66.7	100	4	AAO09783	AAO09783 Human pol
38	36	66.7	107	4	AAO06147	AAO06147 Human pol
39	36	66.7	220	4	ABG26257	ABG26257 Novel hum
40	36	66.7	222	2	AAW55552	AAW55552 H. pylori
41	36	66.7	323	7	ABO67138	ABO67138 Klebsiell
42	36	66.7	412	6	ABU34586	ABU34586 Protein e
43	36	66.7	460	6	ABU36680	ABU36680 Protein e
44	36	66.7	577	7	ADB64994	ADB64994 Human pro
45	36	66.7	646	6	ABU31814	ABU31814 Protein e

RESULT 1
AAW53843 standard; peptide; 10 AA.

AC	XX	AAW53843;
AC	XX	
DT	XX	08-UTL-1998 (first entry)
DE	XX	N-terminus of opoosum LTNP.
XX	XX	
KM	XX	LTNP, lethal toxin neutralising factor; opoosum; envenomation; therapy;
KM	XX	anti-haemorrhagic protein; Elapidae; Vipertidae; sea snake; snake bite;
KM	XX	sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KM	XX	histamine reaction treatment.
OS	XX	Didelphis virginiana.
PN	XX	US5744449-A.
XX	XX	
PD	XX	28-APR-1998.
XX	XX	
PP	XX	03-JUN-1996; 96US-00657163.
XX	XX	
PR	XX	10-MAY-1993; 93US-00056387.
PR	XX	22-SEP-1994; 94US-00310340.
PA	XX	(LIPP/) LIPPS B V.
PA	XX	(LIPP/) LIPPS F W.
PI	XX	Lipps FW, Lipps BV;
DR	XX	WPI, 1998-271108/24.
PT	XX	Lethal Toxin Neutralising Factor peptide from opoosum - can neutralise
XX	XX	venom(s) from all major families of poisonous snakes.
PS	XX	Claim 7, Col 11, lipp: English.

This sequence represents the peptide of the invention. It is a lethal toxin neutralising factor (LTNP) moiety from a 68 kDa anti-haemorrhagic protein derived from an opoosum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Vipertidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 CC
 SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
 |||||
 DB 1 LKAMDPTPPL 10

RESULT 2

ABB80222
 ID ABB80222 standard; peptide; 10 AA.

AC ABB80222;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNP, LT-10.

KM Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KM IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.

OS Synthetic.

PN WO2003060471-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPF/) LIPPS B V.
 (LIPF/) LIPPS F W.

PI LIPPS BV, LIPPS FW;

DR WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

PS Claim 7; Page 3; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
 |||||
 DB 1 LKAMDPTPPL 10

RESULT 3

ABB80226
 ID ABB80226 standard; peptide; 11 AA.

AC ABB80226;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNP, LT-11.

KM Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KM IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.

OS Synthetic.

PN WO2003060471-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPF/) LIPPS B V.
 (LIPF/) LIPPS F W.

PI LIPPS BV, LIPPS FW;

DR WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 4

AB880225
 ID ABB80225 standard; peptide; 12 AA.

AC ABB80225;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNF, LT-12.

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 XX IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 XX ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 XX SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 XX Graves' disease; Addison's disease; Hodgkin's disease; depression;
 XX saliva; ELISA.

OS Synthetic.

XX WO2003060471-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001044.

XX 14-JAN-2002; 2002US-00047945.

XX (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX LIPPS BV, LIPPS FW;

XX WPI; 2003-636703/60.

PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin B (IGB), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 5

AAM11575
 ID AAM11575 standard; peptide; 15 AA.

AC AAM11575;

DT 25-MAR-2003 (revised)

DT 20-MAR-1997 (first entry)

DE N-terminal peptide from lethal toxin neutralising factor.

XX Lethal toxin neutralising factor; LTNF; opoosum; bee toxin;
 XX scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
 XX Didelphis virginiana.

XX US576297-A.

XX 19-NOV-1996.

XX 22-SEP-1994; 94US-00310340.

XX 10-MAY-1993; 93US-00058387.

XX (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX LIPPS BV, LIPPS FW;

XX WPI; 1997-011287/01.

PT Treatment of victims of bee or scorpion stings or plant or bacterial
 PT toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
 PT peptide.

XX Claim 7; Col 9; 9pp; English.

XX The present sequence is from the N-terminus of a 68 kD protein purified
 CC from the serum of the opossum Didelphis virginiana. The full-length
 CC protein is a lethal toxin neutralising factor (LTNF). The use of purified
 CC LTNF or of the chemically synthesised 15mer N-terminal peptide for
 CC treating victims of bee stings, scorpion stings and bacterial or plant
 CC toxins is claimed. The patent disclosure does not provide any evidence
 CC for neutralising activity against these various toxins. There is evidence
 CC of significant neutralising activity of the opossum LTNF and the 15mer
 CC peptide against venom from snakes of the families Crotalidae, Elapidae,
 CC Hydroliidae and Vipridae. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 15 AA;

Query Match 100.0%; Score 54; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 6

AAW53841
 ID AAW53841 standard; peptide; 15 AA.

AC AAW53841;

DT 08-JUL-1998 (first entry)

XX

DE N-terminus of opossum LTNF.

KW LTNF: lethal toxin neutralising factor; opossum; envenomation; therapy;
KW anti-hemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW histamine reaction treatment.

OS Didelphis virginiana.

XX US5744449-A.

XX PN

XX 28-APR-1998.

PD

PP 03-JUN-1996; 96US-00657163.

PP

XX 10-MAY-1993; 93US-00058387.

PR

XX 22-SEP-1994; 94US-00310340.

PR

PA (LIRP/) LIRPS B V.

XX (LIRP/) LIRPS F W.

XX

XX Lirpps FW, Lirpps BV;

PI

XX WPI: 1998-271108/24.

DR

PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
PT venom(s) from all major families of poisonous snakes.

XX

PS Claim 1, Col 11; 11pp; English.

XX

CC This sequence represents the peptide of the invention. It is a lethal
CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-hemorrhagic
CC protein derived from an opossum. The peptide can be used in a method for
CC treating a victim of envenomation from a poisonous snake, preferably a
CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
CC is useful for the treatment of snake bites, sepsis, allergies caused by
CC the environment and treatment of bee or scorpion stings or toxicities
CC caused by plant or bacterial toxins. The peptide can also be used in
CC histamine reaction treatment. The peptide can be used in envenomation
CC treatment for a variety of snakes without prior identification of the
CC snake. Being short it can be synthetically prepared rather than the
CC current production in horses, where some people can show hypersensitivity
CC to horse proteins

CC

SQ Sequence 15 AA;

Query Match 100.0%; Score 54; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 LKAMPTPPL 10
|||||
1 LKAMPTPPL 10

DB

RESULT 7
ABBB0223
ID ABBB0223 standard; peptide; 15 AA.

XX

AC ABBB0223;

XX

XX 06-NOV-2003 (first entry)

DT

XX Synthetic LTNF, LT-15.

DE

XX lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B;
KW IgG; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; achute; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.

XX

OS Synthetic.

[illegible]

PD 24-JUL-2003.
 XX 14-JAN-2003; 2003WO-US001044.
 PF 14-JAN-2002; 2002US-00047945.
 PR (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 XX LIPPS BV, LIPPS FW;
 PI WPI; 2003-636703/60.
 DR Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PS Claim 7; Page 4; 24pp; English.
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 CC
 SQ Sequence 9 AA;
 XX
 XX Query Match 92.6%; Score 50; DB 7; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTP 9
 DB 1 LKAMDPTP 9
 XX
 XX RESULT 9
 XX ID ABB80228 standard; peptide; 8 AA.
 XX AC ABB80228;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 XX Synthetic LTNF, LT-8.
 XX
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KM IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.
 XX
 XX Synthetic.
 XX
 XX WO2003060471-A2.
 XX
 XX 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003WO-US001044.
 XX

XX 14-JAN-2002; 2002US-00047945.
 PR (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 XX LIPPS BV, LIPPS FW;
 PI WPI; 2003-636703/60.
 DR Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PS Claim 7; Page 4; 24pp; English.
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 CC
 SQ Sequence 8 AA;
 XX
 XX Query Match 79.6%; Score 43; DB 7; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTP 8
 DB 1 LKAMDPTP 8
 XX
 XX RESULT 10
 XX ID AAO02179 standard; protein; 94 AA.
 XX AC AAO02179;
 XX
 XX 06-NOV-2001 (first entry)
 XX
 XX Human polypeptide SEQ ID NO 16071.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorders; arthritis; inflammation.
 XX
 XX Homo sapiens.
 OS
 XX WO200164835-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 26-FEB-2001; 2001WO-US004927.
 XX
 XX 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 XX (HYSR-) HYSR INC.
 XX

XX Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI; 2001-514836/56.
 DR N-PSDB; AAI82110.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 16071, 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The which may induce
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 94 AA;
 XX
 Query Match 77.8%; Score 42; DB 4; Length 94;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKAMPPTTP 9
 Db 48 LKSGDPTTP 56
 XX
 RESULT 11
 ABB58900
 ID ABB58900 standard; protein; 165 AA.
 XX
 AC ABB58900;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 3492.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00644150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL03003.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 3492; 21pp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABJ16176-ABJ10511), expressed DNA
 CC sequences (ABL01840-ABJ16175) and the encoded proteins (ABJ57737-
 CC ABJ72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 165 AA;
 XX
 Query Match 75.9%; Score 41; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MDPTTPT 10
 Db 1 MDPTTPT 7
 XX
 RESULT 12
 AAB59012
 ID AAB59012 standard; protein; 459 AA.
 XX
 AC AAB59012;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 720.
 XX
 KW Human; breast cancer; ovarian cancer; cytotoxic; immunosuppressive;
 KW noctropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antitumor; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200055173-A1.
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005881.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-611515/58.
 DR N-PSDB; AAF21915.
 XX
 PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX
 PS Claim 11; Page 1174-1176; 1299pp; English.
 XX
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytotoxic; immunosuppressive; noctropic;
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;

DE Yeast protein kinase #10.

XX Prediction; secondary structure; alignment; evolutionary conservation;
 KW homology; periodicity; co-variation analysis; antigenic site;
 KW site directed mutagenesis; interaction.

XX Saccharomyces cerevisiae.

OS US5958784-A.

PN 28-SEP-1999.

PD 25-MAR-1992; 92US-00857224.

PP 25-MAR-1992; 92US-00857224.

PR (BENN/) BENNER S A.

PA Benner SA;

PI WPI; 1999-570766/48.

DR Predicting the folded structure of proteins.

XX Disclosure; Col 225-228; 113pp; English.

PS Sequences AA43902-Y44015 represent proteins used in a novel method of
 CC predicting the folded structure of proteins, by aligning sequences of
 CC homologous proteins and using patterns of evolutionarily conserved and
 CC varied sequences to assign positions. Positions in the alignment are
 CC assigned to the surface or inside of the folded structure, active sites,
 CC and parsing segments. Secondary structural units are assigned by
 CC identifying periodicity in the assignments, and assembled into globular
 CC form using distance constraints imposed by disulfide bridges, active site
 CC assignments and co-variation analysis. The predicted secondary structures
 CC are useful for identifying antigenic sites on a protein molecule, as
 CC guides for site directed mutagenesis studies, and for understanding the
 CC interaction of a protein with other molecules

XX Sequence 267 AA;

SQ Query Match 70.4%; Score 38; DB 2; Length 267;

Best Local Similarity 70.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 2;

QY 1 LKAMPPTPL 10

Db 31 LKVVDPPTPL 40

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 Job time : 83.4595 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:23:04 ; Search time 67.5676 Seconds
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Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMPPTPL 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	US-10-047-945-1	Sequence 1, Appl1
2	54	100.0	11	US-10-047-945-5	Sequence 5, Appl1
3	54	100.0	12	US-10-047-945-4	Sequence 4, Appl1
4	54	100.0	15	US-10-047-945-2	Sequence 2, Appl1
5	50	92.6	9	US-10-047-945-6	Sequence 6, Appl1
6	43	79.6	8	US-10-047-945-7	Sequence 7, Appl1
7	41	75.9	80	US-10-424-599-253125	Sequence 253125,
8	41	75.9	148	US-10-437-963-133945	Sequence 133945,
9	40	74.1	153	US-10-425-115-235826	Sequence 235826,
10	39	72.2	137	US-10-425-115-276829	Sequence 276829,
11	39	72.2	169	US-10-437-963-162813	Sequence 162813,
12	39	72.2	206	US-10-437-963-162816	Sequence 162816,
13	39	72.2	459	US-09-925-298-720	Sequence 720, App

14	39	72.2	459	14	US-10-102-806-720	Sequence 720, App
15	38	70.4	75	16	US-10-767-701-51220	Sequence 51220, A
16	38	70.4	82	17	US-10-425-115-279472	Sequence 279472, A
17	38	70.4	132	16	US-10-437-963-138037	Sequence 138037, A
18	37	68.5	15	14	US-10-161-791-444	Sequence 444, App
19	37	68.5	54	15	US-10-424-599-158162	Sequence 158162, A
20	37	68.5	67	15	US-10-424-599-273019	Sequence 273019, A
21	37	68.5	117	17	US-10-425-115-363646	Sequence 363646, A
22	37	68.5	126	17	US-10-425-115-307337	Sequence 307337, A
23	37	68.5	210	9	US-09-071-035-232	Sequence 232, App
24	37	68.5	210	14	US-10-206-576-232	Sequence 232, App
25	37	68.5	244	16	US-10-437-963-179361	Sequence 179361, A
26	37	68.5	256	9	US-09-071-035-230	Sequence 230, App
27	37	68.5	256	14	US-10-206-576-230	Sequence 230, App
28	37	68.5	270	15	US-10-282-122A-57118	Sequence 57118, A
29	37	68.5	285	15	US-10-282-122A-56870	Sequence 56870, A
30	37	68.5	367	16	US-10-437-963-146546	Sequence 146546, A
31	37	68.5	481	14	US-10-369-493-7817	Sequence 7817, Ap
32	37	68.5	732	17	US-10-425-115-204968	Sequence 204968, A
33	37	68.5	736	15	US-10-425-114-68941	Sequence 68941, A
34	36	66.7	34	16	US-10-437-963-127940	Sequence 127940, A
35	36	66.7	52	17	US-10-425-115-279389	Sequence 279389, A
36	36	66.7	79	17	US-10-425-115-244806	Sequence 244806, A
37	36	66.7	126	16	US-10-437-963-135430	Sequence 135430, A
38	36	66.7	128	17	US-10-425-115-330144	Sequence 330144, A
39	36	66.7	128	17	US-10-425-115-361942	Sequence 361942, A
40	36	66.7	139	15	US-10-424-599-280103	Sequence 280103, A
41	36	66.7	204	16	US-10-437-963-190433	Sequence 190433, A
42	36	66.7	222	15	US-10-335-977-6879	Sequence 8979, Ap
43	36	66.7	231	16	US-10-767-701-56593	Sequence 56593, A
44	36	66.7	253	17	US-10-425-115-367927	Sequence 367927, A
45	36	66.7	412	15	US-10-282-122A-62510	Sequence 62510, A

ALIGNMENTS

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RESULT 1
US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BIRNIE V
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN B
; FILE REFERENCE: FMLPATO15US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1
```

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 2
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

```

```

Query Match          100.0%; Score 54; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPPL 10
        |||||
Db      1 LKAMDPTPPL 10

```

```

RESULT 3
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

```

```

Query Match          100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPPL 10
        |||||
Db      1 LKAMDPTPPL 10

```

```

RESULT 4
US-10-047-945-2
; Sequence 2, Application US/10047945

```

```

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
US-10-047-945-2

```

```

Query Match          100.0%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPPL 10
        |||||
Db      1 LKAMDPTPPL 10

```

```

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

```

```

Query Match          92.6%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPPL 9
        |||||
Db      1 LKAMDPTPPL 9

```

```

RESULT 6
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

```

```
APPLICANT: LIPPS, BIRNIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
FILE REFERENCE: FMP1PAT015US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIORITY FILING DATE:
PRIORITY FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7
```

```
Query Match
Best Local Similarity 79.6%; Score 43; DB 14; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8
```

```
RESULT 7
US-10-424-599-253125
Sequence 253125, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253125
LENGTH: 80
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_70598C.1.pap
US-10-424-599-253125
```

```
Query Match
Best Local Similarity 75.9%; Score 41; DB 15; Length 80;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 LKAMDPTP 10
DB 62 LKGTDPPTPV 71
```

```
RESULT 8
US-10-437-963-133945
Sequence 133945, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
```

```
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 133945
LENGTH: 148
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(148)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4577_14658C.1.pap
US-10-437-963-133945
```

```
Query Match
Best Local Similarity 75.9%; Score 41; DB 16; Length 148;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LKAMDPTP 10
DB 42 LKRDPTP 51
```

```
RESULT 9
US-10-425-115-235826
Sequence 235826, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 235826
LENGTH: 153
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(153)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_14658C.1.pap
US-10-425-115-235826
```

```
Query Match
Best Local Similarity 74.1%; Score 40; DB 17; Length 153;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 LKAMDPTP 10
DB 62 LKAMDPTP 71
```

```
RESULT 10
US-10-425-115-276829
Sequence 276829, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
```

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 276829
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_184050C.1.pep
US-10-425-115-276829

Query Match
Best Local Similarity 72.2%; Score 39; DB 17; Length 137;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPPTPL 10
DB 125 AMSDPPL 132

RESULT 11
US-10-437-963-162813
; Sequence 162813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162813
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(169)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61869C.1.pep
US-10-437-963-162813

Query Match
Best Local Similarity 72.2%; Score 39; DB 16; Length 169;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPPTPL 10
DB 61 LSSIDPSPL 70

RESULT 12
US-10-437-963-162816
; Sequence 162816, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
```

```

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162816
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(206)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61871C.1.pep
US-10-437-963-162816

Query Match
Best Local Similarity 72.2%; Score 39; DB 16; Length 206;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPPTPL 10
DB 67 LSSIDPSPL 76

RESULT 13
US-09-925-298-720
; Sequence 720, Application US/09925298
; Publication No. US2002003764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 720
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-720

Query Match
Best Local Similarity 72.2%; Score 39; DB 9; Length 459;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPPTPL 9
DB 346 LRSQDPTPL 354

RESULT 14
US-10-102-806-720
; Sequence 720, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
```



```

FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 720
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-720

```

```

Query Match          72.2%; Score 39; DB 14; Length 459;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPP 9
        |::|
        346 LKSDPTPP 354

```

```

RESULT 15
US-10-767-701-51220
Sequence 51220; Application US/10767701
Publication No. US2004012684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 51220
LENGTH: 75
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: LIB3481-060-Q6-K1-D12.pap
US-10-767-701-51220

```

```

Query Match          70.4%; Score 38; DB 16; Length 75;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPP 9
        |::|
        2 LKTMDDPTPP 10

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Search completed: January 6, 2005, 10:44:42
 Job time : 68.5676 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:09:51 ; Search time 20.2703 Seconds
(without alignments)
32.717 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAMPTPL 10

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA: *
1: /cgn2_6/prodata/1/aa/5A COMB pep: *
2: /cgn2_6/prodata/1/aa/5B COMB pep: *
3: /cgn2_6/prodata/1/aa/5A COMB pep: *
4: /cgn2_6/prodata/1/aa/5B COMB pep: *
5: /cgn2_6/prodata/1/aa/5A COMB pep: *
6: /cgn2_6/prodata/1/aa/5B COMB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	1	US-08-657-163A-2
2	54	100.0	15	1	US-08-310-340A-1
3	54	100.0	15	1	US-08-657-163A-1
4	41	75.9	253	4	US-09-270-767-43223
5	38	70.4	267	2	US-07-857-824B-42
6	37	68.5	15	3	US-08-602-999A-444
7	37	68.5	15	4	US-09-500-124-444
8	37	68.5	210	4	US-09-071-035-232
9	37	68.5	256	4	US-09-071-035-230
10	37	68.5	221	4	US-09-134-000C-6676
11	37	68.5	306	4	US-09-134-000C-6583
12	36	66.7	333	4	US-09-489-039A-13655
13	36	66.7	338	4	US-09-248-796A-20624
14	35	64.8	27	4	US-09-270-767-57016
15	35	64.8	206	4	US-09-538-092-166
16	35	64.8	315	1	US-08-571-758-12
17	35	64.8	315	1	US-08-909-984A-12
18	35	64.8	315	1	US-08-909-984A-12
19	35	64.8	323	4	US-09-248-796A-16328
20	35	64.8	346	1	US-08-276-151-5
21	35	64.8	405	4	US-09-489-039A-9126
22	35	64.8	405	4	US-08-276-151-2
23	35	64.8	648	1	US-08-185-282-1
24	35	64.8	648	1	US-08-185-282-2
25	35	64.8	648	1	US-08-185-282-3
26	35	64.8	648	1	US-08-185-282-4
27	35	64.8	648	1	US-08-185-282-5

28	35	64.8	648	1	US-08-185-282-12	Sequence 12, Appl
29	35	64.8	648	2	US-08-886-751A-6	Sequence 6, Appl
30	35	64.8	648	3	US-09-209-668-13	Sequence 13, Appl
31	35	64.8	648	3	US-08-971-207-1	Sequence 1, Appl
32	35	64.8	648	4	US-08-207-954-3	Sequence 3, Appl
33	35	64.8	657	4	US-09-653-465B-2	Sequence 2, Appl
34	35	64.8	826	4	US-09-894-998A-47	Sequence 47, Appl
35	35	64.8	1068	1	US-08-537-210A-2	Sequence 2, Appl
36	35	64.8	1068	3	US-09-113-825-2	Sequence 2, Appl
37	35	64.8	1078	1	US-08-264-534-32	Sequence 32, Appl
38	35	64.8	1078	1	US-08-083-590A-11	Sequence 11, Appl
39	35	64.8	1078	1	US-08-465-500-32	Sequence 32, Appl
40	35	64.8	1078	2	US-08-346-128-32	Sequence 32, Appl
41	35	64.8	1078	3	US-08-532-384-11	Sequence 11, Appl
42	35	64.8	1078	3	US-08-893-828-32	Sequence 32, Appl
43	35	64.8	2289	3	US-09-051-019-2	Sequence 2, Appl
44	35	64.8	2548	3	US-09-172-422-1	Sequence 1, Appl
45	35	64.8	2556	1	US-08-185-432-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
SYNTHETIC LIPNS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BERLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMPPTPL 10
DB 1 LKAMPPTPL 10

RESULT 2
US-08-310-340A-1
Sequence 1, Application US/08310340A
Patent No. 5576297

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLONE:
LIBRARY:
PUBLICATION INFORMATION:

AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
ISSUE: SINGAPORE
PAGES: 104
DATE: 3-8 NOV 1991

US-08-310-340A-1

Query Match 100.0%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMPPTPL 10
DB 1 LKAMPPTPL 10

RESULT 3
US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 5744449

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA

```

STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIBELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMS AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1

```

```

Query Match      100.0%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPL 10
      |||||
Db      1 LKAMDPTPL 10

```

```

RESULT 4
US-09-270-767-43223
; Sequence 43223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; FILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; TITLE REFERENCES: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43223
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43223

```

```

Query Match      75.9%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 MDPTPL 10
      |||||
Db      43 MDPTPL 49

```

```

RESULT 5
US-07-857-224B-42
; Sequence 42, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich

```

```

STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein Kinase; Table 8 Column 48
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-42

```

```

Query Match      70.4%; Score 38; DB 2; Length 267;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPL 10
      |||||
Db      31 LKAMDPTPL 40

```

```

RESULT 6
US-08-602-999A-444
; Sequence 444, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUTILAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Penile & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-444

Query Match 68.5%; Score 37; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 5 RALPPTPL 13

RESULT 7
US-09-500-124-444
Sequence 444, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-444

Query Match 68.5%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 5 RALPPTPL 13

RESULT 8
US-09-071-035-232
Sequence 232, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-232

Query Match 68.5%; Score 37; DB 4; Length 210;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 24 KPTDPTPL 32

RESULT 9
US-09-071-035-230
Sequence 230, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: G.H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIA TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ. ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-230

Query Match 68.5%; Score 37; DB 4; Length 256;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 50 KPTDPTPI 58

RESULT 10
US-09-134-000C-6676
Sequence 6676, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ. ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6676
LENGTH: 291
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6676

Query Match 68.5%; Score 37; DB 4; Length 291;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 70 KPTDPTPI 78

RESULT 11
US-09-134-000C-6583
Sequence 6583, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ. ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6583
LENGTH: 306
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6583

Query Match 68.5%; Score 37; DB 4; Length 306;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 70 KPTDPTPI 78

RESULT 12
US-09-489-039A-13655
Sequence 13655, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ. ID NOS: 14342
SEQ ID NO 13655
LENGTH: 323
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13655

Query Match 66.7%; Score 36; DB 4; Length 323;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAMDPTPL 9
DB 6 KAMDALPP 14

RESULT 13
US-09-248-796A-20624
Sequence 20624, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
FILE REFERENCE: 107196.132

```
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 20624
/ LENGTH: 338
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-20624
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Query Match          66.7%; Score 36; DB 4; Length 338;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 KAMDPTPPL 10
      |||||
Db      88 KAKDPTDPL 96
```

```
RESULT 14
US-09-270-767-57016
/ Sequence 57016, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 57016
/ LENGTH: 27
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-57016
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Query Match          64.8%; Score 35; DB 4; Length 27;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 LKAMDPTPP 9
      |||||
Db      19 LRPLDPSPP 27
```

```
RESULT 15
US-09-538-092-166
/ Sequence 166, Application US/09538092
/ Patent No. 6753314
/ GENERAL INFORMATION:
/ APPLICANT: Glot, Loic
/ APPLICANT: Mansfield, Traci A.
/ TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
/ FILE REFERENCE: 15966-542
/ CURRENT APPLICATION NUMBER: US/09/538,092
/ CURRENT FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/127,352
/ PRIOR FILING DATE: 1999-04-01
/ PRIOR APPLICATION NUMBER: 60/178,965
/ PRIOR FILING DATE: 2000-02-01
/ NUMBER OF SEQ ID NOS: 1387
/ SOFTWARE: CurataseqFormatter Version 0.9
/ SEQ ID NO 166
/ LENGTH: 206
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
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```
/ OTHER INFORMATION: Polypeptide Accession Number YDRL67W
US-09-538-092-166
```

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Query Match          64.8%; Score 35; DB 4; Length 206;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      1 LKAMDPTPPL 10
      |||||
Db      78 LKAMDSTPPI 87
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Search completed: January 6, 2005, 10:25:05
Job time : 21.2703 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:21; Search time 23.5135 Seconds
(without alignments) 61.380 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLMKTRE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	75.0	237	2 A42013	alpha-1-B-glycopro
2	46	54.8	1213	2 A54063	TATA-binding prote
3	44	52.4	695	2 E75099	hypothetical prote
4	44	52.4	777	2 T38769	hypothetical prote
5	44	52.4	1337	2 T09402	immunoglobulin-lik
6	43	51.2	341	2 AB0644	probable glycosyl
7	43	51.2	687	2 D86314	hypothetical prote
8	43	51.2	932	2 A31898	hydroxymethylgluta
9	42	50.0	115	2 D71194	hypothetical prote
10	42	50.0	398	2 A81717	conserved hypobhe
11	42	50.0	453	2 T04646	aspartate transami
12	42	50.0	564	1 VHXPMV	major structural n
13	42	50.0	662	2 A29900	fasciclin 1 precur
14	41	48.8	151	1 S30146	ribosomal protein
15	41	48.8	339	2 JCS882	myocyte enhancer f
16	41	48.8	349	2 JCS881	myocyte enhancer f
17	41	48.8	411	2 AE2152	two-component sens
18	41	48.8	707	2 F86925	probable acyl-CoA
19	41	48.8	967	2 S58360	antibiotic Peps b
20	41	48.8	975	2 T03004	exodeoxyribonuclea
21	41	48.8	1172	2 T00065	hypothetical prote
22	41	48.8	1559	2 T07757	probable DNA (cyto
23	40	47.6	97	2 S59888	C4 protein - tomat
24	40	47.6	205	2 S26854	microfilament sheat
25	40	47.6	205	2 A40525	proline-rich sheat
26	40	47.6	209	2 B40049	virc-region hypoch
27	40	47.6	209	2 T43565	type III secretion
28	40	47.6	210	2 S21428	hypothetical prote
29	40	47.6	225	2 C70045	two-component resp

30	40	47.6	231	2 F69977	two-component resp
31	40	47.6	309	2 H72626	probable 2-oxoacid
32	40	47.6	337	2 A97084	uncharacterized pr
33	40	47.6	406	2 C83867	Xaa-Pro dipeptidas
34	40	47.6	422	2 D86446	hypothetical prote
35	40	47.6	560	2 T02404	probable beta-gluc
36	40	47.6	609	2 S65208	probable membrane
37	40	47.6	1184	2 D86387	probable protein P
38	40	47.6	1215	2 E70614	hypothetical prote
39	40	47.6	3570	2 T45025	mucin MUC5B, trach
40	39.5	47.0	365	2 F87552	dpn protein [impo
41	39.5	47.0	631	2 A57286	probable serine/th
42	39	46.4	242	2 AD1928	hypothetical prote
43	39	46.4	256	1 WMBEPN	28k protein - suid
44	39	46.4	258	2 T23957	hypothetical prote
45	39	46.4	268	2 S31010	gene 65 protein -

ALIGNMENTS

RESULT 1

A42013 alpha-1-B-glycoprotein - North American opossum (fragments)

C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)

C>Date: 10-Jul-1992 #sequence_rev1stion 10-Jul-1992 #ext_change 09-Jul-2004

C/Accession: A42013

R/Catanesse, J.J.; Kresse, L.F.

Biochemistry 31, 410-418, 1992

A>Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hu

A/Reference number: A42013; MID:92118834; PMID:1731898

A/Accession: A42013

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-237 <CAT>

A/Cross-references: UNIPROT:Q28359; GB:J05356

C/Keywords: glycoprotein

Query Match 75.0%; Score 63; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.0095;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMKTRE 15
Db 1 LKAMDPTPLMKTRE 15

RESULT 2

A54063 TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C>Date: 02-Aug-1994 #sequence_rev1stion 02-Aug-1994 #ext_change 09-Jul-2004

C/Accession: A54063

R/Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.

Science 264, 933-941, 1994

A>Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to

A/Reference number: A54063; MID:94233377; PMID:8178153

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1213 <VER>

A/Cross-references: UNIPROT:Q24325; GB:X79243; NID:G541664; PIDN:CA55830.1; PID:G54166

A/Gene: FlyBase:Taf150

C/Genetics:

A/Gene: FlyBase:Taf150

A/Cross-references: FlyBase:FBgn0011836

Query Match 54.8%; Score 46; DB 2; Length 1213;
Best Local Similarity 53.3%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMKTRE 15
Db 620 LSAMDSPVLMIRLD 634

RESULT 3

hypotheetical protein PAB1590 - *Pyrococcus abyssi* (strain Orsay)
C/Species: *Pyrococcus abyssi*
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: E75099
R/anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A/Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
A/Reference number: A75001
A/Accession: E75099
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-695 <KAM>
A/Cross-references: UNIPROT:Q9UZG1, GB:AJ248286, GB:AL096836, NID:g5458366, PIDN:CAB5005
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: PAB1590

Query Match 52.4%; Score 44; DB 2; Length 695;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPPLPWIK 13
DB 561 ANDPKPMMLE 571

RESULT 4

hypotheetical protein SPAC3H8.11 - fission yeast (*Schizosaccharomyces pombe*)
C/Species: *Schizosaccharomyces pombe*
C/Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004
C/Accession: T38769, T38072
R/Genetics: S. J. Churcher, C. M. J. Barrell, B. G. J. Rajandream, M. A. J. Walsh, S. V.
submitted to the EMBL Data Library, January 1996
A/Reference number: Z21810
A/Accession: T38769
A/Molecule type: DNA
A/Residues: 1-105 <GEN>
A/Cross-references: UNIPROT:Q10146, EMBL:Z69086, NID:g1177658, PIDN:CAA93168.1; PID:g117
A/Experimental source: strain 972h-; cosmid c3H8
R/Connor, R. J. Churcher, C. M. J. Barrell, B. G. J. Rajandream, M. A. J. Walsh, S. V.
submitted to the EMBL Data Library, April 1996
A/Reference number: Z21767
A/Accession: T38072
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 90-777 <CON>
A/Cross-references: EMBL:Z70690, NID:g1256511, PIDN:CAA94619.1, PID:g3859771, GSPDB:GNOC
A/Experimental source: strain 972h-; cosmid c1F3
C/Genetics:
A/Gene: SPAC1F3.01; SPDB:SPAC3H8.11; SPDB:SPAC1F3.01
A/Map position: 1

Query Match 52.4%; Score 44; DB 2; Length 777;
Best Local Similarity 46.2%; Pred. No. 41;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPPLPWIKT 15
DB 212 SVDETEBIWSTB 224

RESULT 5

Immunoglobulin-like protein IGSP1 - human
C/Species: *Homo sapiens* (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09402
R/Mazzarella, R. J. Pengue, G. J. Jones, J. J. Jones, C. J. Schlessinger, D.

Genomics 48, 157-162, 1998

A/Title: Cloning and expression of an immunoglobulin superfamily gene (IGSP1) in Xg25.

A/Reference number: Z16665, MUID:98190514, PMID:9521868

A/Accession: T09402

A/Status: preliminary, translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1327 <MAZ>

A/Cross-references: UNIPROT:O15070, EMBL:AF034198, NID:g2645889, PIDN:ACG52057.1, PID:g2

C/Genetics:

A/Gene: 1g6f1

A/Map position: Xg25

Query Match 52.4%; Score 44; DB 2; Length 1327;
Best Local Similarity 63.6%; Pred. No. 75;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPPPLWIKT 14
DB 25 MDPPPLWIKT 35

RESULT 6

probable glycosyl hydrolase STY1249 [imported] - *Salmonella enterica* subsp. *enterica* ser
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A/Note: this species has also been called *Salmonella typh*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB0644
R/Parkhill, J. J. Dougan, G. J. James, K. D. J. Thomson, N. R. J. Pickard, D. J. Wain, J. J. Churcher,
th, T. J. Connor, P. J. Cronin, A. J. Davis, P. J. Davies, R. M. J. Dowd, L. J. White, N. J. Farrar,
S. J. Mouton, S. J. O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C. J. Quail, M. J. Rutherford, K. J. Simmonds, M. J. Skelton, J. J. Stevens, K. J.
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB0644
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-341 <PAR>
A/Cross-references: GB:AL513382, PIDN:CMD0833.1, PID:g16502378, GSPDB:GN00176
C/Genetics:
A/Gene: STY1249

Query Match 51.2%; Score 43; DB 2; Length 341;
Best Local Similarity 47.1%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KANDPPLPWIKT 14
DB 217 RAIDPRPAGSPFWIKT 233

RESULT 7

hypotheetical protein P2H15.14 - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
C/Accession: D86314
R/Theologis, A. J. Ecker, J. R. J. Palm, C. J. J. Federspiel, N. A. J. Kaul, S. J. White, O. J. Alonso,
Chin, C. W. J. Chung, M. K. J. Conn, L. J. Conway, A. B. J. Conway, A. R. J. Creasey, T. H. J. Dewar, K. J.
ansen, N. F. J. Hughes, B. J. Hultine, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J. L. J. Jenkins, J. J. Johnson-Hopson, C. J. Khan, S. J. Khaykin, E. J. Kim, C.
C. A. J. Li, J. H. J. Li, Y. J. Lin, X. J. Liu, S. X. J. Liu, Z. A. J. Luce, J. S. J. Maiti, R. J. Marziani,
Rizzo, M. J. Rooney, T. J. Rowley, D. J. Sakano, H.
A/Authors: Salzberg, S. L. J. Schwartz, J. R. J. Shin, P. J. Southwick, A. M. J. Sun, H. J. Tallon,
ker, M. J. Wu, D. J. Yu, G. J. Fraser, C. M. J. Venter, J. C. J. Davis, R. W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A86141; MUID:21016719, PMID:11130712
A/Accession: D86314
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-687 <STO>

A/Cross-references: UNIPROT:Q9JMT8; GB:AE051172; NID:9665069; PIDN:AAF97271.1; GSPDB:GN
C/Genetics:
A/Map position: 1
C/Superfamily: homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 51.2%; Score 43; DB 2; Length 687;
Best Local Similarity 46.7%; Pred. No. 52;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKADPTPLMKT 15
Db 225 LRLLQNEPLMKT 239

RESULT 8
A/Accession: A31898
C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A31898; A28367
R/Woodward, H.D.; Allen, J.M.C.; Lemariz, W.J.
J. Biol. Chem. 263, 18411-18418, 1988
A/Title: 3-hydroxy-3-methylglutaryl-CoA reductase of the sea urchin embryo. Deduced
A/Reference number: A31898; PMID:89054023; PMID:3192541
A/Accession: A31898
A/Molecule type: mRNA
A/Residues: 1-932 <MO>
A/Cross-references: UNIPROT:P16393; GB:J04200; NID:9161522; PIDN:AAA30060.1; PID:9161523
A/Note: the authors rearranged portions of the coding region in Figure 2, and the above
submitted to GenBank

A/Note: the authors translated the codon GGA for residue 805 as Glu
R/Woodward, H.D.; Allen, J.M.C.; Lemariz, W.J.
J. Biol. Chem. 263, 2513-2517, 1988
A/Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is de
A/Reference number: A28367; PMID:8115403; PMID:3276692
A/Accession: A28367
A/Molecule type: mRNA
A/Residues: 689-735 <MO>
C/Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t
C/Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C/Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N
F;279,850,886,930/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 51.2%; Score 43; DB 1; Length 932;
Best Local Similarity 70.0%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KADPTPLM 11
Db 298 KRIDPTPLM 307

RESULT 9
D71194
hypothetical protein PH1828 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C/Accession: D71194
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hattawa, Y.; Hino, Y.; Yamamoto, S.; Seki
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A/Reference number: A71000; PMID:98344137; PMID:9679194
A/Accession: D71194
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-115 <KAM>
A/Cross-references: UNIPROT:O59492; GB:AP000007; NID:93236134; PIDN:BA30947.1; PID:93235
A/Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1828

Query Match 50.0%; Score 42; DB 2; Length 115;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLM 12
Db 89 ISBSPPLM 97

RESULT 10
A81717
conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain N19g)
C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81717
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gilm, M.; Nelson, W.; Debby, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; PMID:20150255; PMID:10684935
A/Accession: A81717
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-398 <TET>
A/Cross-references: UNIPROT:Q9PPL02; GB:AE002298; GB:AE002160; NID:97190343; PIDN:AAF3917
A/Experimental source: strain N19g (MoPn)
C/Genetics:
A/Gene: TC0306
C/Superfamily: Chlamydia trachomatis hypothetical protein CT036

Query Match 50.0%; Score 42; DB 2; Length 398;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KADPTPL 10
Db 309 KRIDPTPL 317

RESULT 11
T04646
aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana
N/Alternate names: aspartate aminotransferase; protein P10N7.200
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C/Accession: T04646; S56657; S47490
R/Bevan, M.; Rose, M.; Hempel, S.; Bittan, K.D.; Hobeisel, J.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
A/Reference number: Z15263
A/Accession: T04646
A/Molecule type: DNA
A/Residues: 1-453 <BEV>
A/Cross-references: UNIPROT:P46248; EMBL:AL021636
A/Experimental source: cultivar Columbia; BAC clone P10N7
R/Wilkie, S.B.; Roper, J.M.; Smith, A.G.; Warren, M.V.
Plant Mol. Biol. 27, 1227-1233, 1995
A/Title: Isolation, characterization and expression of a cDNA clone encoding plastid aspa
A/Reference number: S56657; PMID:95284373; PMID:7766905
A/Accession: S56657
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-21, 'NV', 24-453 <WIL>
A/Cross-references: EMBL:X81026; NID:9531554; PIDN:CAA56932.1; PID:9531555
C/Genetics:
A/Gene: aat1
A/Map position: 4
A/Genome: nuclear
A/Intons: 20/3; 37/3; 102/3; 115/3; 145/3; 182/1; 218/3; 266/3; 322/2; 410/3
A/Note: P10N7.200
C/Superfamily: aspartate aminotransferase
C/Keywords: aminotransferase; chloroplast; phosphoprotein; pyridoxal phosphate
F;298/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 50.0%; Score 42; DB 2; Length 453;
 Best Local Similarity 60.0%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLMIK 13
 :|||:
 Db 238 IDPPEQWVK 247

RESULT 12

VHXPMV

major structural nucleoprotein - Machupo virus
 N/Alternate names: nucleocapsid protein

C/Species: Machupo virus

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C/Accession: S18042

R/Griffiths, C.; Wilson, S.M.; Clegg, J.C.S.

A/Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship w

A/Reference number: S18042

A/Accession: S18042

A/Molecule type: genomic RNA

A/Residues: 1-564 <GRI>

A/Cross-references: UNIPROT:P26578; EMBL:X62616; NID:g60621; PIDN:CAA44486.1; PID:g60622

C/Genetics:

A/Map position: segment 8

C/Superfamily: arenavirus major nucleoprotein

C/Keywords: nucleocapsid; nucleoprotein

Query Match 50.0%; Score 42; DB 1; Length 564;
 Best Local Similarity 46.7%; Pred. No. 60;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIK 15
 :|||:
 Db 368 VKKLDPTNLTJLDIR 382

RESULT 13

A29900

fasciclin I precursor - American bird grasshopper

C/Species: Schistocerca americana (American bird grasshopper)

C/Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 09-Jul-2004

C/Accession: A29900; A31817

R/Zinn, K.; McAllister, L.; Goodman, C.S.

Cell 53, 577-587, 1988

A/Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Dro

A/Reference number: A29900; MUID:88223351; PMID:3370670

A/Accession: A29900

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-662 <ZIN>

A/Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847

R/Show, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Baestianl, M.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988

A/Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t

A/Reference number: A94202; MUID:88276943; PMID:2833842

A/Accession: A31817

A/Molecule type: mRNA

A/Residues: 25-42 <SNO>

A/Cross-references: EMBL:M20544; EMBL:J03787

Query Match 50.0%; Score 42; DB 2; Length 662;
 Best Local Similarity 58.3%; Pred. No. 72;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMI 12
 :|||:
 Db 104 LSEIDGNPLMI 115

RESULT 14

S30146
 ribosomal protein S13, cytosolic - maize

C/Species: Zea mays (maize)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: S30146

R/Jocain, P.; Giot, C.; Phillips, G.

Plant Mol. Biol. 21, 701-704, 1993

A/Title: cDNA nucleotide sequence and expression of a maize cytoplasmic ribosomal protei

A/Reference number: S30146; MUID:93192530; PMID:8446368

A/Accession: S30146

A/Molecule type: mRNA

A/Residues: 1-151 <JOA>

A/Cross-references: UNIPROT:Q05761; EMBL:X62455; NID:g286058; PIDN:CAA44311.1; PID:g2860

C/Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology

C/Keywords: protein biosynthesis; ribosome

F/2-151/Product: ribosomal protein S13 #status predicted <MAT>

F/82-148/Domains: eubacterial ribosomal protein S15 homology <ES15>

Query Match 48.8%; Score 41; DB 1; Length 151;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPLMIK 14
 :|||:
 Db 21 TPPTWLKT 28

RESULT 15

JC5882

myocyte enhancer factor 2B-2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 09-Jul-2004

C/Accession: JC5882

R/Moriaki, T.; Seramvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Moriaki, H.;

J. Biochem. 122, 939-946, 1997

A/Title: Mouse Mef2b gene: Unique member of MEF2 gene family.

A/Reference number: JC5881; MUID:98104045; PMID:9443808

A/Accession: JC5882

A/Molecule type: DNA

A/Residues: 1-339 <MOR>

A/Cross-references: UNIPROT:Q05087; DDBJ:D87828

C/Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.

C/Genetics:

A/Gene: Mef2b

A/Map position: 8

F/2-57/Domains: serum response factor DNA-binding domain homology <SRF>

Query Match 48.8%; Score 41; DB 2; Length 339;
 Best Local Similarity 61.5%; Pred. No. 50;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLMIK 15
 :|||:
 Db 281 ASPPTPVSIXS 293

Search completed: January 6, 2005, 10:23:48
 Job time : 25.5135 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:00:35 ; Search time 128.514 Seconds
(without alignments)
67.157 Million cell updates/sec

Title: US-10-047-945-2

Sequence: 1 LKAMDPTPLWIKTB 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	17	2 Q9TR78	Q9TR78 didelphis m
2	84	100.0	291	1 DM43_DIDMR	P82957 didelphis m
3	75	89.3	140	2 Q8H275	Q8H275 didelphis m
4	75	89.3	291	2 Q8H274	Q8H274 didelphis m
5	63	75.0	314	2 Q8HYX5	Q8HYX5 didelphis m
6	52	61.9	504	2 Q8MIS3	Q8MIS3 didelphis m
7	50	59.5	227	2 Q73ZB2	Q73ZB2 mycobacteri
8	50	59.5	227	2 AAS04008	AAS04008 mycobacte
9	48	57.1	344	2 Q7MTQ9	Q7MTQ9 porphyromon
10	47	56.0	51	2 Q8FNB0	Q8FNB0 corynebacte
11	47	56.0	351	1 Y4VU_RHISN	C53218 rhizobium s
12	46	54.8	370	2 Q7OE48	Q7OE48 anopheles g
13	46	54.8	634	2 Q9VOP3	Q9VOP3 drosophila
14	46	54.8	854	2 Q9VOP4	Q9VOP4 drosophila
15	46	54.8	856	2 Q9G210	Q9G210 drosophila
16	46	54.8	1017	2 Q7KU30	Q7KU30 drosophila
17	46	54.8	1017	2 AAS64617	AAS64617 drosophila
18	46	54.8	1221	1 TAF2_DRCMB	Q24325 drosophila
19	45	53.6	97	2 Q9IME9	Q9IME9 chilla leaf
20	45	53.6	97	2 Q91P83	Q91P83 tomato leaf
21	45	53.6	128	2 Q833V1	Q833V1 enterococcu
22	45	53.6	312	2 Q9N126	Q9N126 bos taurus
23	45	53.6	467	2 Q7YQ77	Q7YQ77 sus scrofa
24	45	53.6	477	2 Q18150	Q18150 caenorhabdi
25	44	52.4	125	2 Q9NVE1	Q9NVE1 homo sapien
26	44	52.4	242	2 Q8NVE5	Q8NVE5 homo sapien
27	44	52.4	242	2 Q8BXK6	Q8BXK6 mus musculu
28	44	52.4	287	2 Q8H272	Q8H272 didelphis m
29	44	52.4	287	2 Q8H273	Q8H273 didelphis m
30	44	52.4	377	2 Q92T32	Q92T32 rhizobium m
31	44	52.4	695	2 Q9UZG1	Q9UZG1 pyrococcus

32	44	52.4	777	1 YD81_SCHPO	Q10146 echizosacch
33	44	52.4	1305	1 RRP1_ANSV9	Q70695 african hor
34	44	52.4	137	2 Q15070	Q15070 homo sapien
35	43	51.2	78	2 Q7NFI1	Q7NFI1 glisobacter
36	43	51.2	205	2 Q82TE1	Q82TE1 nitrosomona
37	43	51.2	278	2 Q946H8	Q946H8 oryza sativ
38	43	51.2	278	2 Q6ERU5	Q6ERU5 oryza sativ
39	43	51.2	286	2 Q7VZ12	Q7VZ12 bordetella
40	43	51.2	286	2 Q7W5Y0	Q7W5Y0 bordetella
41	43	51.2	286	2 Q7WGN4	Q7WGN4 bordetella
42	43	51.2	341	1 NAGZ_SALTY	Q82716 salmonella
43	43	51.2	341	1 NAGZ_SALTY	Q82716 salmonella
44	43	51.2	354	2 Q8VM74	Q8VM74 rhizobium s
45	43	51.2	360	2 Q846T8	Q846T8 myxococcus

ALIGNMENTS

RESULT 1
ID Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE ANTI-BOTROPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_Taxid=9268;
RN [1]
RP SEQUENCE.
RA MEDLINE=95149299; PubMed=7846694;
RX Perales J., Moussetache H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-botrophic complex
from the serum of South American Didelphidae.";
RL Toxicon 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CBS5FB40E73B2A2A CRC64;
Query Match 100.0%; Score 84; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLWIKTB 15
Db 1 LKAMDPTPLWIKTB 15
RESULT 2
ID DM43_DIDMR STANDARD; PRT; 291 AA.
AC P82957;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_Taxid=9268;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RX MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.,
Makino D.L., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -I- FUNCTION: Metalloproteinase inhibitor.
CC -I- SUBUNIT: Homodimer.
CC -I- TISSUE SPECIFICITY: Blood and milk.

```
CC -1- PTM: N-glycosylated.
CC -1- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011015; LEM_1like.
DR Pfam: PF00047; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79 IG-like V-type 1.
FT DOMAIN 114 171 IG-like V-type 2.
FT DOMAIN 191 288 IG-like V-type 3.
FT DISULFID 28 74 Potential.
FT DISULFID 121 163
FT DISULFID 213 265
FT CARBOHYD 23 265 N-linked (GlcNAc...) (potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (potential).
FT CARBOHYD 175 175 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 291 AA; 32390 MW; 17A496227B69A65B CRC64;

Query Match 100.0%; Score 84; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
DB 1 LKAMDPTPLMIKTE 15

RESULT 3
08H275 PRELIMINARY; PRT; 140 AA.
AC 08H275;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP51-D (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
ON NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131000; AAN06911.1; -.
DR InterPro: IPR011015; LEM_1like.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

Query Match 89.3%; Score 75; DB 2; Length 140;
Best Local Similarity 93.3%; Pred. No. 0.0006;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
DB 42 LKAMDPTPLMIKTE 56

RESULT 4
08H274 PRELIMINARY; PRT; 291 AA.
AC 08H274;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP14 (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
```

```
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131001; AAN06912.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011015; LEM_1like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 291 291
SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;

Query Match 89.3%; Score 75; DB 2; Length 291;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
DB 1 LKAMDPTPLMIKTE 15

RESULT 5
08HYX5 PRELIMINARY; PRT; 314 AA.
AC 08HYX5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Venom metalloproteinase inhibitor DM43D precursor.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
ON NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tringilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C.,
RA Dumont G.B., Ho P.L., Perales J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163806; AAN64698.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 314 Venom metalloproteinase inhibitor DM43b.
SQ SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;

Query Match 75.0%; Score 63; DB 2; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
DB 24 LKAMDPTPLMIKTE 38

RESULT 6
08MIS3 PRELIMINARY; PRT; 504 AA.
AC 08MIS3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Venom mycotoxin inhibitor DM64 precursor.
OS Didelphis marsupialis (Southern opossum).
```

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metachetia; Didelphimorphia; Didelphidae; Didelphis.
 NCBI_TaxID=9268;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22361219; PubMed=12473101;
 RA Rocha S.L., Lomonte B., Neves-Ferreira A.G., Trugilho M.R.,
 Junqueira-De-Azevedo Id I., Ho P.L., Domont G.B., Gutierrez J.M.,
 Perales J.;
 "Functional analysis of DM64, an anti-myotoxic protein with
 immunoglobulin-like structure from *Didelphis marsupialis* serum.";
 RT Eur. J. Biochem. 269:6052-6062(2002).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Rocha S.L.G., Neves-Ferreira A.G.C., Trugilho M.R.O.,
 Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J.;
 RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY078384; MAL82794.1; -.
 DR HSSP; P24071; IUCT.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR011015; LEM-like.
 DR Pfam; PF000647; IG_3.
 DR SMART; SM00409; IG_3.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 KW Signal.
 FT SIGNAL
 FT CHAIN 25 504
 SQ SEQUENCE 504 AA; 55975 MW; 046529A6CBA63B9 CRC64;

Query Match 61.9%; Score 52; DB 2; Length 504;
 Best local Similarity 66.7%; Pred. No. 10;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMITE 15
 DB 24 LKAMETPLMITE 38

RESULT 7
 Q73ZB2 PRELIMINARY; PRT; 227 AA.
 AC Q73ZB2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=MAP1691C;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium avium complex (MAC).
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017233; AAS04008.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0EB199 CRC64;

Query Match 59.5%; Score 50; DB 2; Length 227;
 Best local Similarity 72.7%; Pred. No. 9.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
 DB 146 LKALDPRPLM 156

RESULT 8
 AAS04008 PRELIMINARY; PRT; 227 AA.
 ID AAS04008;
 AC AAS04008;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN MAP1691C.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017233; AAS04008.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0EB199 CRC64;

Query Match 59.5%; Score 50; DB 2; Length 227;
 Best local Similarity 72.7%; Pred. No. 9.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
 DB 146 LKALDPRPLM 156

RESULT 9
 Q7MTQ9 PRELIMINARY; PRT; 344 AA.
 ID Q7MTQ9;
 AC Q7MTQ9;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Rhodanese-like domain protein.
 GN OrderedLocNames=PG1887;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22629867; PubMed=12949112;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 Haft D.H., Kolonay J.F., Nelson W.C., Maeson T.M., Tallon L., Gray J.,
 Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 Dewhirst F.E., Fraser C.M.;
 "Complete genome sequence of the oral pathogenic bacterium
 Porphyromonas gingivalis strain W83.";
 RT J. Bacteriol. 185:5591-5601(2003).
 RL EMBL; AB017178; AA066871.1; -.
 DR TIGR; PG1887; -.
 DR GO; GO:0004792; P:thiosulfate sulfotransferase activity; IEA.
 DR GO; GO:0008772; P:sulfate transport; IEA.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Thiosulfatrans.
 DR Pfam; PF00581; Rhodanese; 1.
 DR PROSITE; PS00380; RHODANES_1; 1.
 DR PROSITE; PS0206; RHODANES_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 344 AA; 38572 MW; F3D938CD668BF04 CRC64;

Query Match 57.1%; Score 48; DB 2; Length 344;
 Best local Similarity 46.7%; Pred. No. 29;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMITE 15

Db 199 LSACDPNRP1WVSE 213

RESULT 10

Q8RNB0 PRELIMINARY; PRT; 51 AA.

AC O8FNB0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE Hypoetical protein.
 GN OrderedLocustNames=C82235;
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VS-314;
 RX MEDLINE=22723752; PubMed=12840036;
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
 RA Gojobori T.;
 RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens.";
 RL Genome Res. 13:1572-1579 (2003).
 DR EMBL; AF005221; BAC19045.1;
 KW Complete proteome; Hypoetical protein.
 SQ SEQUENCE 51 AA; 5686 MW; 759F3C5BDCCE414A CRC64;

Query Match 56.0%; Score 47; DB 2; Length 51;
 Best Local Similarity 50.0%; Pred. No. 5.6;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMPPTPLWIKT 14
 Db 21 SLDPTRVWERT 32

RESULT 11
 Y4VU RHISN STANDARD; PRT; 351 AA.
 AC 053218;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypoetical 39.2 kDa protein y4vU.
 GN ORFNames=y4vU;
 OS Rhizobium sp. (strain NGR234).
 OC Plasmid sym pNGR234.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes.";
 RN Nature 387:394-401 (1997).
 RP SEQUENCE OF 1-279 FROM N.A.
 RX MEDLINE=96389014; PubMed=8796346;
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
 RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 RT NGR234 using dye terminators and a thermostable 'sequenase': a
 RT beginning.";
 RL Genome Res. 6:590-600 (1996).
 CC -1- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
 CC family.
 CC -----

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DR EMBL; Z68203; CA92425.1; -.
 DR EMBL; AE000101; AA891898.1; -.
 DR InterPro; IPR002103; Bac_Luciferase.
 DR InterPro; IPR011251; Luciferase_Like.
 DR Pfam; PF00296; Bac_Luciferase; 1.
 KW Hypoetical protein; Monooxygenase; Oxidoreductase; Plasmid.
 SQ SEQUENCE 351 AA; 39158 MW; 86BDE3B8A40C8D CRC64;

Query Match 56.0%; Score 47; DB 1; Length 351;
 Best Local Similarity 77.8%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPPLWIKT 14
 Db 167 PTPPLWIKT 175

RESULT 12

Q7Q848 PRELIMINARY; PRT; 370 AA.

AC Q7Q848;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE AGCP7225 (Fragment).
 GN Name=agcG51396; ORFNames=ENSANGS0000004288;
 OS Anopheles gambiae str. PEST.
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 2 C2 domains.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; AA80100848; EAA07048.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008021; C:synaptic vesicle; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002149; Alatroxin_recept.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PROSITE; PSS0004; C2_DOMAIN_2; 2.
 RN NON TER 1
 SQ SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD08F CRC64;

Query Match 54.8%; Score 46; DB 2; Length 370;
 Best Local Similarity 54.5%; Pred. No. 66;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKANDPTPLW 11

Db 294 IRALDPTPLW 304

RESULT 13

Q9VQP3 PRELIMINARY; PRT; 634 AA.

Q9VQP3
 AC Q9VQP3;

DT 01-MAY-2000 (TREMBlRel. 13, Created)

DT 01-OCT-2002 (TREMBlRel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBlRel. 26, Last annotation update)

DE CG3327-pB.

GN Name=E23; ORFNames=CG3327;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

OC Ephyridioidae, Drosophilidae, Drosophila.

OX NCBI_TaxID=7227;

RP [1]

RP SEQUENCE FROM N.A.

RX MedLine=22426006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amentides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Gabor G.L.,

RA Abrial J.F., Asgarian A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Baughn A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Bernon B.P., Bhandal D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck Y., Brockstein P., Broctier P.,

RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dubin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,

RA Fioder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glocker A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,

RA Jostai M., Kalush F., Karpen G.H., Ke Z., Kemtson J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Mektoulov G., Milshina N.V., Mobery C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,

RA Palazzolo M., Petlan G.S., Pan S., Pollard J., Puti V., Reese M.G.,

RA Renkert K., Remington K., Saunders R.D., Scheel F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,

RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zhang R.A., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RL "The genome sequence of Drosophila melanogaster.";

RL Science 287:1185-1195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MedLine=22426055; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavertry T., Muzny D.M., Nelson C.R.,

RA Paclab J.M., Pak S., Pfeiffer B.D., Richards S., Sodergren E.D.,

RA Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G.G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;

RL "Finishing a whole-genome shotgun: release 3 of the Drosophila

RL melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MedLine=22426070; PubMed=12537573;

RA Kaulin J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,

RA Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RL "The transposable elements of the Drosophila melanogaster euchromatin:

RL a genomic perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RL [4]

Thu Jan 6 10:59:27 2005

us-10-047-945-2.open.rup

Page 7

Search completed: January 6, 2005, 10:17:46
Job time : 131.514 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:08:37 ; Search time 119.189 Seconds
(without alignments)
45.146 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLMKITE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	2 AAM1575	AAM1575 N-termina
2	84	100.0	15	2 AAM53841	AAM53841 N-terminu
3	84	100.0	15	7 ABB80223	ABB80223 Synthetic
4	69	82.1	12	7 ABB80225	ABB80225 Synthetic
5	65	77.4	11	7 ABB80226	ABB80226 Synthetic
6	54	64.3	10	2 AAM53843	AAM53843 N-terminu
7	54	64.3	10	7 ABB80222	ABB80222 Synthetic
8	50	59.5	9	7 ABB80227	ABB80227 Synthetic
9	47	56.0	303	4 ABB81844	ABB81844 Novel hum
10	47	56.0	31	6 ABR54218	ABR54218 Human NOV
11	46	54.8	267	3 AAY74721	AAY74721 Neisseria
12	46	54.8	267	3 AAY74718	AAY74718 Neisseria
13	46	54.8	729	4 ABB59797	ABB59797 Drosophila
14	46	54.8	1189	2 AAR56496	AAR56496 TARA-bind
15	46	54.8	1213	2 AAM06086	AAM06086 Drosophila
16	46	54.8	1213	2 AAM25029	AAM25029 TARA-bind
17	46	54.8	1219	4 ABB62618	ABB62618 Drosophila
18	45	53.6	137	7 ADH88053	ADH88053 Enterococ
19	45	53.6	267	3 AAY74720	AAY74720 Neisseria
20	45	53.6	312	6 ABU65528	ABU65528 Bovine ph
21	44	52.4	37	4 ABB42105	ABB42105 Peptide #
22	44	52.4	37	4 AAM75798	AAM75798 Human bon
23	44	52.4	37	4 AAM62985	AAM62985 Human bra
24	44	52.4	76	3 AAG54516	AAG54516 Zee may
25	44	52.4	79	3 AAG54515	AAG54515 Zee may

ALIGNMENTS

RESULT 1	AAM1575	AAM1575 standard; peptide, 15 AA.
AC	XX	XX
DT	25-MAR-2003 (revised)	
DT	20-MAR-1997 (first entry)	
DE	N-terminal peptide from lethal toxin neutralising factor.	
KM	Lethal toxin neutralising factor; LTNF, Opossum; bee toxin;	
KM	scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.	
OS	Didelphis virginiana.	
XX	XX	XX
PN	US5576297-A.	
PD	19-NOV-1996.	
PF	22-SBP-1994; 9AUS-00310340.	
PR	10-MAY-1993; 9AUS-00058387.	
PA	(LIPF/) LIPPS B V.	
PA	(LIPF/) LIPPS F W.	
PI	Lipps FW, Lipps BV;	
DR	WPI; 1997-011287/01.	
XX	XX	XX
PT	Treatment of victims of bee or scorpion stings or plant or bacterial	
PT	toxins - by admin. of lethal toxin-neutralising factor or its N-terminal	
XX	peptide.	
PS	Claim 7; Col 9; pp; English.	
XX	XX	XX
CC	The present sequence is from the N-terminus of a 68 kD protein purified	
CC	from the serum of the opossum <i>Didelphis virginiana</i> . The full-length	
CC	protein is a lethal toxin neutralising factor (LTNF). The use of purified	
CC	LTNF or of the chemically synthesised 15mer N-terminal peptide for	
CC	treating victims of bee stings, scorpion stings and bacterial or plant	
CC	toxins is claimed. The patent disclosure does not provide any evidence	
CC	for neutralising activity against these various toxins. There is evidence	
CC	of significant neutralising activity of the opossum LTNF and the 15mer	
CC	peptide against venom from snakes of the families Crotalidae, Elapidae,	
CC	Hydroiidae and Viperidae. (Updated on 25-MAR-2003 to correct pf field.)	
XX	XX	XX

26	44	52.4	92	3 AAG54605	AAG54605 Zee may
27	44	52.4	95	3 AAG54604	AAG54604 Zee may
28	44	52.4	120	4 AAO10737	AAO10737 Human pol
29	44	52.4	125	4 AAB93318	AAB93318 Human pro
30	44	52.4	156	4 ABB22890	ABB22890 Novel hum
31	44	52.4	242	7 ADB90591	ADB90591 Human pit
32	44	52.4	299	7 ADB90617	ADB90617 Human pit
33	44	52.4	1336	6 ABR47496	ABR47496 Breast ca
34	44	52.4	1336	8 ADP18673	ADP18673 Human pro
35	44	52.4	1457	4 AAU52796	AAU52796 Novel hum
36	43	51.2	8	7 ABB80228	ABB80228 Synthetic
37	43	51.2	286	6 ABU23550	ABU23550 Protein e
38	43	51.2	316	4 ABB23871	ABB23871 Novel hum
39	43	51.2	341	6 ABU47234	ABU47234 Protein e
40	43	51.2	341	6 ABU45098	ABU45098 Protein e
41	43	51.2	341	6 ABU47970	ABU47970 Protein e
42	43	51.2	393	4 AAM79784	AAM79784 Human pro
43	43	51.2	496	3 AAG27883	AAG27883 Arabidops
44	43	51.2	522	3 AAG27882	AAG27882 Arabidops
45	43	51.2	687	3 AAG27881	AAG27881 Arabidops

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
 |||||
 DB 1 LKAMDPTPLMIKTE 15

RESULT 2

AAM53841

ID AAM53841 standard; peptide; 15 AA.

XX AAM53841;

XX 08-JUL-1998 (first entry)

XX N-terminus of opossum LTNP.

XX LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.

XX Didelphis virginiana.

XX US5744449-A.

XX 28-APR-1998.

XX 03-JUN-1996; 96US-00657163.

XX 10-MAY-1993; 93US-00058387.

XX 22-SEP-1994; 94US-00310340.

XX (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX LIPPS FW, LIPPS BV;

XX WPI; 1998-271108/24.

XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.

XX Claim 1, Col 11; 11pp; English.

XX This sequence represents the peptide of the invention. It is a lethal
 CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
 |||||
 DB 1 LKAMDPTPLMIKTE 15

RESULT 3

ID ABB80223 standard; peptide; 15 AA.

XX ABB80223;

XX 06-NOV-2003 (first entry)

XX Synthetic LTNP, LT-15.

XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX Synthetic.

XX WO2003060471-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001044.

XX 14-JAN-2002; 2002US-00047945.

XX (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX LIPPS BV, LIPPS FW;

XX WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 3; Page 3; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGF levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKTE 15
 |||||
 DB 1 LKAMDPTPLMIKTE 15

RESULT 4

ABB80225

ID ABB80225 standard; peptide; 12 AA.
 XX ABB80225;
 AC
 XX
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX
 DE Synthetic LTNF, LT-12.
 XX
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 XX
 PN WO2003060471-A2.
 XX
 XX 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003WO-US001044.
 XX
 XX 14-JAN-2002; 2002US-00047945.
 XX
 XX (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 XX
 XX LIPPS BV, LIPPS FW;
 PI
 XX
 DR WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PS Claim 7; Page 4; 24pp; English.
 XX
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 82.1%; Score 69; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00038; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLMI 12
 |||||
 Db 1 LKAMDPTPLMI 12
 |||||
 RESULT 5
 ABB80226
 ID ABB80226 standard; peptide; 11 AA.
 XX
 AC ABB80226;

XX
 DT 06-NOV-2003 (first entry)
 XX
 XX
 DE Synthetic LTNF, LT-11.
 XX
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 XX
 PN WO2003060471-A2.
 XX
 XX 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003WO-US001044.
 XX
 XX 14-JAN-2002; 2002US-00047945.
 XX
 XX (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 XX
 XX LIPPS BV, LIPPS FW;
 PI
 XX
 DR WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IGF, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PS Claim 7; Page 4; 24pp; English.
 XX
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 77.4%; Score 65; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLM 11
 |||||
 Db 1 LKAMDPTPLM 11
 |||||
 RESULT 6
 AAW53843
 ID AAW53843 standard; peptide; 10 AA.
 XX
 AC AAW53843;
 XX
 XX 08-JUL-1998 (first entry)
 XX

PD 24-JUL-2003.
 XX 14-JAN-2003; 2003MO-US001044.
 PF 14-JAN-2002; 2002US-00047945.
 PR 14-JAN-2002; 2002US-00047945.
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX LIPPS BV, LIPPS FW;
 PI LIPPS BV, LIPPS FW;
 XX WPI; 2003-636703/60.
 DR Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 9 AA;
 Query Match 59.5%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPP 9
 DB 1 LKAMDPTPP 9
 RESULT 9
 ID ABB818144 standard; protein; 303 AA.
 XX ABB818144;
 AC ABB818144;
 XX 18-FEB-2002 (first entry)
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18135.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX

PA (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS62331.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 48503; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probe, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostic as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABB00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 303 AA;
 Query Match 56.0%; Score 47; DB 4; Length 303;
 Best Local Similarity 42.9%; Pred. No. 34;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 KAMDPTPPMIXTE 15
 DB 39 EASDPVPYVRRLQ 52
 RESULT 10
 ID ABR54218 standard; protein; 531 AA.
 XX ABR54218;
 AC ABR54218;
 XX 23-JUN-2003 (first entry)
 DT 23-JUN-2003 (first entry)
 XX
 DE Human NOV21a protein SEQ ID NO:104.
 XX
 KM Human; NOVX; anticholesterol; hypotensive; cardiant; dermatological;
 KM anorectic; immunosuppressive; cytostatic; antidiabetic; anti-infectivity;
 KM haemostatic; anti-inflammation; antiaesthetic; anti-HIV; immunomodulator;
 KM neuroprotective; nociceptive; antiparkinsonian; metabolic; antilipemic;
 KM gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
 KM congenital heart defect; aortic stenosis; valve disease; transplantation;
 KM tuberous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
 KM prostate cancer; metabolic disorder; neoplasia; lymphoma; uterus cancer;
 KM fertility; haemophilia; hypercoagulation; graft versus host disease;
 KM idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
 KM Crohn's disease; multiple sclerosis; infectious disease; cancer;
 KM cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
 KM immune disorder; haematopoietic disorder; dyslipidaemia;
 KM metabolic syndrome X.
 XX
 OS Homo sapiens.

XX MO2003023001-A2.
 XX
 XX 20-MAR-2003.
 XX
 XX 09-SEP-2002; 2002WO-US028538.
 XX
 PR 07-SEP-2001; 2001US-0318120P.
 PR 07-SEP-2001; 2001US-0318184P.
 PR 10-SEP-2001; 2001US-0318430P.
 PR 17-SEP-2001; 2001US-0322636P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 17-SEP-2001; 2001US-0322816P.
 PR 19-SEP-2001; 2001US-0322817P.
 PR 19-SEP-2001; 2001US-0323519P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 20-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324969P.
 PR 25-SEP-2001; 2001US-0325091P.
 PR 26-SEP-2001; 2001US-0324990P.
 PR 14-DEC-2001; 2001US-0341144P.
 PR 26-FEB-2002; 2002US-0359599P.
 PR 05-MAR-2002; 2002US-0361663P.
 PR 03-MAY-2002; 2002US-0377908P.
 PR 17-MAY-2002; 2002US-0381483P.
 PR 29-MAY-2002; 2002US-0383863P.
 PR 02-JUL-2002; 2002US-0393332P.
 PR 17-JUL-2002; 2002US-0396412P.
 PR 13-AUG-2002; 2002US-0403517P.
 PR 06-SEP-2002; 2002US-00236417.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PI Agee ML, Alsbrook JP, Anderson DW, Berghs C, Boldog FL,
 PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A,
 PI Crabtree J, DiPippo VA, Edinger SR, Eissen AD, Ellerman K,
 PI Gangoli EA, Gerlach VL, Glot L, Gorman L, Guo X, Gussev VY, Ji W,
 PI Kexuda R, Khrantsov NV, Leach MD, Lepley DW, Li L, Liu X,
 PI Malvanekar UM, Miller CE, Ooi CE, Ort T, Padigara M, Patunajan M,
 PI Pena CE, Rieger DK, Rothenberg ME, Shenoy SG, Shinkets RA,
 PI Spaderna SK, Szytek KA, Taupier RJ, Twonlow N, Vernet CM, Voss EZ,
 PI Zernusen BD, Zhong M,
 DR MPI; 2003-313241/30.
 XX N-PSDB; ACC62287.
 PT Novel human proteins and nucleic acid encoding the proteins, useful for
 PT diagnosis, treatment and prevention of disorders involving the human
 PT protein or nucleic acid e.g. cardiac and neurological disorders.
 XX
 PS Claim 1; Page 173; 460pp; English.
 XX
 CC The present invention describes isolated human NOVX proteins, where X is
 CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
 CC ABR54167 to ABR54276. NOVX sequences have antithrombotic, cardiac,
 CC hyperosmotic, dermatological, anorectic, immunosuppressive, cytostatic,
 CC antidiabetic, antifertility, haemostatic, antiinflammatory, anti-HIV,
 CC antitumoric, metabolic, immunomodulator, neuroprotective, nootropic,
 CC antiparasitism and antipneumatic activities, and can be used in gene
 CC therapy. NOVX proteins are useful for treating or preventing a pathology
 CC associated with a NOVX protein in humans and for treating a syndrome
 CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
 CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
 CC valve disease, tuberculous sclerosis, scleroderma, obesity, transplantion,
 CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
 CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
 CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
 CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
 CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX

CC sequences, which are used in examples from the present invention.
 CC ABR54277 represents a human trypsinogen protein given in comparison with
 CC the human NOV35b protein in the exemplification of the present invention
 XX
 SQ Sequence 531 AA;
 Query Match 56.0%; Score 47; DB 6; Length 531;
 Best Local Similarity 66.7%; Pred. No. 61;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 MDPTPLMKTKE 15
 Db 70 MDTSPPLMTLLE 81
 RESULT 11
 ID AAY74721 standard; protein; 267 AA.
 AC AAY74721;
 DT 21-MAR-2000 (first entry)
 DE Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:916.
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy.
 OS Neisseria meningitidis.
 XX
 XX WO957280-A2.
 XX
 XX 11-NOV-1999.
 XX
 XX 30-APR-1999; 99WO-US009346.
 XX
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
 PI Petersen J, Piazza M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
 PI Tettelin H, Venter JC,
 DR MPI; 2000-062150/05.
 XX N-PSDB; AA253483.
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX
 PS Claim 2; Page 555; 1453pp; English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to Neisserial
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC Neisseria bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be

CC used in gene therapy protocols
XX

Sequence 267 AA:

Query Match 54.8%; Score 46; DB 3; Length 267;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKT 14
DB 9 AKHPPTPLWLOT 20

RESULT 12

AAV74718 standard; protein; 267 AA.

AAV74718;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:910.

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
antibacterial; gene therapy.

Neisseria meningitidis.

MO957280-A2.

11-NOV-1999.

30-APR-1999; 99MO-US009346.

01-MAY-1998; 98US-0083758P.

31-JUL-1998; 98US-0094669P.

02-SEP-1998; 98US-0098984P.

02-SEP-1998; 98US-0099062P.

09-OCT-1998; 98US-0103749P.

09-OCT-1998; 98US-0103796P.

25-FEB-1999; 99US-0121528P.

(CHIR) CHIRON CORP.

(GENO-) INST GENOMIC RES.

Frazer C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,

Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M,

Tetzelin H, Venter JC;

WPI; 2000-062150/05.

N-PSDB; AA253480.

Novel Neisserial polypeptides predicted to be useful antigens for

vaccines and diagnostics.

Claim 2; Page 553; 1453pp; English.

AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941

represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides

CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent

PCR primers used in the exemplification of the present invention. The

polypeptides, the polynucleotides, antibodies and compositions of the

invention can be used as vaccines, as diagnostic reagents, and as

immunogenic compositions. The polypeptides can be used in the manufacture

of medicaments for treating or preventing infection due to Neisserial

bacteria (e.g. meningitis and septicemia), to detect the presence of

Neisseria bacteria, or to raise antibodies. They may also be used to

screen for agonists or antagonists, which may themselves have use as

antibacterial agents. The polynucleotides of the invention may also be

used in gene therapy protocols

Sequence 267 AA:

Query Match 54.8%; Score 46; DB 3; Length 267;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKT 14
DB 9 AKHPPTPLWLOT 20

RESULT 13

ABBS9797 standard; protein; 729 AA.

ABBS9797;

26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 6183.

Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001MO-US009231.

23-MAR-2000; 2000US-0191637P.

11-JUL-2000; 2000US-00614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;

WPI; 2001-656860/75.

N-PSDB; ABL03900.

New isolated nucleic acid detection reagent for detecting 1000 or more

genes from Drosophila and for elucidating cell signalling and cell-cell

interactions.

Disclosure; SEQ ID NO 6183; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent

capable of detecting 1000 or more genes from Drosophila. The invention is

useful in developmental biology and in elucidating cell signalling and

cell-cell interactions in higher eukaryotes for the development of

insecticides, therapeutics and pharmaceutical drugs. The invention

discloses genomic DNA sequences (ABL01840-ABL01875), expressed DNA

sequences (ABL01840-ABL01875) and the encoded proteins (ABBS7737

ABBS7072). The sequence data for this patent did not form part of the

printed specification, but was obtained in electronic format directly

from WPI at ftp.wipo.int/pub/published_pct_sequences

Sequence 729 AA;

Query Match 54.8%; Score 46; DB 4; Length 729;

Best Local Similarity 57.1%; Pred. No. 1.2e+02;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKT 14

DB 689 LKQNSTSEPLWIKT 702

RESULT 14

AAAS6496

ID AAAS6496 standard; protein; 1189 AA.

```

XX AC AAR56496;
XX DE
XX DT 25-MAR-2003 (revised)
XX DT 23-MAR-1995 (first entry)
XX DE TATA-binding protein-associated factor dTAFI50.
XX KM TATA-binding protein associated factor; dTAFI50; screening; diagnostic;
XX KW therapeutic; gene transcription regulation.
XX OS Drosophila.
XX FH Key Location/Qualifiers
XX FT Misc-difference 923
XX FT /note= "Val or Leu"
XX FT Misc-difference 1106
XX FT /note= "Arg, Pro or His"
XX FT Misc-difference 1172
XX FT /note= "STOP"
XX FT Misc-difference 1176
XX FT /note= "STOP"
XX PN WO9417087-A1.
XX PD 04-AUG-1994.
XX PF 28-JAN-1994; 94WO-US001114.
XX PR 28-JAN-1993; 93US-00013412.
XX PR 30-JUN-1993; 93US-00087119.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tjian R, Comai L, Dynlacht BD, Hoey T, Rupert S, Tanese N;
XX PI Wang E, Weinzierl ROJ;
XX DR WPI; 1994-264019/32.
XX DR N-PSDB; AAQ70733.
XX PT TATA-binding protein associated protein factors - and corresponding
XX PT nucleotide sequence and deriv. antibodies, useful in screening,
XX PT diagnostics and therapeutics.
XX PS Disclosure; Page 156; 180pp; English.
XX CC The TATA-binding protein associated factor hTAFI50 (including specific
XX CC antibodies and fusion products) are used in drug screening, diagnostics
XX CC and therapeutics. They are used in the development of specific
XX CC biochemical assays for screening compounds that agonise or antagonise
XX CC selected transcription factors involved in regulating gene expression
XX CC associated with human pathology. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 1189 AA;

Query Match 54.8%; Score 46; DB 2; Length 1189;
Best Local Similarity 53.3%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPPIWIKTE 15
DB 589 LSAMDDSPVLMIRLD 603

RESULT 15
AAW06086
ID AAW06086 standard; protein; 1213 AA.
XX AAW06086;
AC
XX
XX 25-MAR-2003 (revised)
DT 27-JAN-1997 (first entry)

```

```

XX DE Drosophila TATA-binding protein associated factor dTAFI150 protein.
XX KM Drosophila; TATA-binding protein; TBP associated factor; TFIID;
XX KM RNA polymerase II; transcription; messenger RNA; nuclear fraction;
XX KW holoenzyme; lambda-gc11; expression library.
XX OS Drosophila melanogaster.
XX PN US5534410-A.
XX PD 09-JUL-1996.
XX PF 28-JAN-1994; 94US-00188582.
XX PR 28-JAN-1993; 93US-00013412.
XX PR 30-JUN-1993; 93US-00087119.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Comai L, Hoey T, Tanese N, Rupert S, Weinzierl ROJ, Tjian R;
XX PI Wang E, Dynlacht BD;
XX DR WPI; 1996-333245/33.
XX DR N-PSDB; AAT42219.
XX PT Screen for cpds. that bind human TATA-binding protein associated factor -
XX PT by testing ability to bind to polypeptide fragments of the factor, useful
XX PT as (ant)agonists of transcription factors involved in disease.
XX PS Example; Col 123-132; 86pp; English.
XX CC This is the amino acid sequence of the Drosophila TATA-binding protein
XX CC (TBP) associated factor (TAP) designated TAFI160. The protein is a
XX CC component of the TFIID fraction required for reconstituting RNA
XX CC polymerase II in vitro transcription activity. The encoded protein has an
XX CC estimated mol. wt. of 60 KD by SDS-PAGE. The invention relates to
XX CC purified proteins involved in transcription by RNA polymerase II
XX CC polymerase which transcribes messenger RNA. RNA polymerase II
XX CC transcription proceeds in vitro upon addition of several nuclear
XX CC fractions designated TFIID, B, D, E, F, H, I and J to RNA polymerase II
XX CC holoenzyme. Fraction TFIID has been shown to contain a TBP and other
XX CC TAFs. Purification of TFIID and separation of its components reveals
XX CC proteins ranging in size from 30-250 KD. Serum raised against the TFIID
XX CC fraction allowed cloning of the corresp. genes from lambda-gc11
XX CC expression libraries. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 1213 AA;

Query Match 54.8%; Score 46; DB 2; Length 1213;
Best Local Similarity 53.3%; Pred. No. 2.1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPPIWIKTE 15
DB 620 LSAMDDSPVLMIRLD 634

Search completed: January 6, 2005, 10:22:47
Job time : 123.189 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:23:04 ; Search time 101.351 Seconds
(without alignments)
53.365 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84
Sequence: 1 LKAMDPTPLPWIKTE 15

Scoring table: BLASTSUM62
Gap 10.0, Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep.*
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6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	US-10-047-945-2	Sequence 2, Appl1
2	69	82.1	12	US-10-047-945-4	Sequence 4, Appl1
3	65	77.4	11	US-10-047-945-5	Sequence 5, Appl1
4	54	64.3	10	US-10-047-945-1	Sequence 1, Appl1
5	50	59.5	9	US-10-047-945-6	Sequence 6, Appl1
6	50	59.5	73	US-10-425-115-223175	Sequence 223175,
7	47	56.0	15	US-10-425-115-223175	Sequence 104, App
8	46	54.8	85	US-10-424-599-278038	Sequence 278038,
9	46	54.8	103	US-10-425-115-228625	Sequence 228625,
10	46	54.8	384	US-10-437-963-200494	Sequence 200494,
11	45	53.6	41	US-10-424-599-173148	Sequence 173148,
12	45	53.6	312	US-09-885-303A-16	Sequence 16, Appl
13	44	52.4	37	US-09-864-761-45331	Sequence 45331, A

14	44	52.4	70	US-10-424-599-229035	Sequence 229035,
15	44	52.4	95	US-10-425-115-287756	Sequence 287756,
16	44	52.4	106	US-10-424-599-255201	Sequence 255201,
17	44	52.4	124	US-10-424-599-151167	Sequence 151167,
18	44	52.4	144	US-10-424-599-205702	Sequence 205702,
19	44	52.4	150	US-10-425-115-303133	Sequence 303133,
20	44	52.4	151	US-10-425-115-257569	Sequence 257569,
21	44	52.4	151	US-10-425-115-257569	Sequence 257569,
22	44	52.4	156	US-10-739-930-8506	Sequence 8506, Ap
23	44	52.4	158	US-10-425-114-63058	Sequence 63058, A
24	44	52.4	530	US-10-424-599-283741	Sequence 283741,
25	44	52.4	1336	US-10-177-293-228	Sequence 228,
26	43	51.2	8	US-10-047-945-7	Sequence 7, Appl1
27	43	51.2	68	US-10-425-115-251177	Sequence 251177,
28	43	51.2	115	US-10-425-115-322493	Sequence 322493,
29	43	51.2	129	US-10-437-963-168841	Sequence 168841,
30	43	51.2	156	US-10-437-963-114167	Sequence 114167,
31	43	51.2	258	US-10-437-963-197262	Sequence 197262,
32	43	51.2	278	US-10-437-963-197265	Sequence 197265,
33	43	51.2	286	US-10-282-122A-51474	Sequence 51474, A
34	43	51.2	341	US-10-282-122A-73022	Sequence 73022, A
35	43	51.2	341	US-10-282-122A-75158	Sequence 75158, A
36	43	51.2	341	US-10-282-122A-75894	Sequence 75894, A
37	43	51.2	840	US-10-437-963-144200	Sequence 144200,
38	43	51.2	932	US-10-041-018-220	Sequence 220, App
39	42	50.0	82	US-10-437-963-128480	Sequence 128480,
40	42	50.0	91	US-10-424-599-264272	Sequence 264272,
41	42	50.0	105	US-10-425-115-345889	Sequence 345889,
42	42	50.0	117	US-10-425-115-185330	Sequence 185330,
43	42	50.0	136	US-10-767-701-54623	Sequence 54623, A
44	42	50.0	140	US-10-425-115-202626	Sequence 202626,
45	42	50.0	147	US-10-425-115-228366	Sequence 228366,

ALIGNMENTS

RESULT 1
US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FMLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLPWIKTE 15
DB 1 LKAMDPTPLPWIKTE 15

RESULT 2
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 82.1%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPLM 12
DB 1 LKAMDPTPTPLM 12

RESULT 3
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 77.4%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPLM 11
DB 1 LKAMDPTPTPLM 11

RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
US-10-047-945-1

Query Match 64.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPL 10
DB 1 LKAMDPTPTPL 10

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 59.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTP 9
DB 1 LKAMDPTPTP 9

RESULT 6
US-10-425-115-223175
; Sequence 223175, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 223175
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135126C.1.pcp
US-10-425-115-223175
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Query Match          59.5%; Score 50; DB 17; Length 73;
Best Local Similarity 53.3%; Pred. No. 6.1;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 LKMDPTPLWKTE 15
Db      51 LAGDPRPKWKTE 65
```

```
RESULT 7
US-10-236-417-104
; Sequence 104, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 104
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-104
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Query Match          56.0%; Score 47; DB 15; Length 531;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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QY      4 MDPTPLWKTE 15
Db      70 MDTPPLWKTE 81
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RESULT 8
US-10-424-599-278038
; Sequence 278038, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278038
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93091C.1.pcp
US-10-424-599-278038
```

```
Query Match          54.8%; Score 46; DB 15; Length 85;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 TPPLWKTE 15
Db      45 TPPLWKTE 53
```

```
RESULT 9
US-10-425-115-228625
; Sequence 228625, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 228625
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140098C.1.pcp
US-10-425-115-228625
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Query Match          54.8%; Score 46; DB 17; Length 103;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      7 TPPLWKTE 14
Db      50 TPPLWKTE 57
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```
RESULT 10
US-10-437-963-200494
; Sequence 200494, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200494
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95958C.1.pcp
US-10-437-963-200494
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Query Match          54.8%; Score 46; DB 16; Length 384;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 3 AMDPPLPWIKT 14
DB 91 AAAPPLMLRT 102
```

```

RESULT 11
US-10-424-599-173148
; Sequence 173148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173148
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127369C.1.pcp
US-10-424-599-173148
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```

Query Match          53.6%; Score 45; DB 15; Length 41;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 5 DPTPLWIKTE 15
DB 14 DPTPLWMAQPE 24
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```

RESULT 12
US-09-885-303A-16
; Sequence 16, Application US/09885303A
; Publication No. US20030032078A1
; GENERAL INFORMATION:
; APPLICANT: TRAVIS, GABRIEL H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF MACULAR
; FILE REFERENCE: UTSD: 758US
; CURRENT APPLICATION NUMBER: US/09/885,303A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/263,837
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; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-885-303A-16
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Query Match          53.6%; Score 45; DB 10; Length 312;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LKAMDPTPLWIKT 14
DB 268 LKAMDPSGLYVRT 281
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RESULT 13
US-09-864-761-45321
; Sequence 45321, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45321
; LENGTH: 37
; TYPE: PRT
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:09:51 ; Search time 30.4054 Seconds

(Without alignments)
32.717 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84
Sequence: 1 LKAMPPTPLMKTR 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
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- 4: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
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- 6: /cgn2_6/prodata/1/aa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	1 US-08-310-340A-1	Sequence 1, Appl1
2	84	100.0	15	1 US-08-657-163A-1	Sequence 1, Appl1
3	84	64.3	10	1 US-08-657-163A-2	Sequence 2, Appl1
4	46	54.8	1213	1 US-08-188-582-20	Sequence 20, Appl1
5	46	54.8	1213	1 US-08-646-715-20	Sequence 20, Appl1
6	45	53.6	137	4 US-09-134-000C-5938	Sequence 5938, Ap
7	42	50.0	910	4 US-10-140-002-112	Sequence 112, App
8	41	48.8	151	4 US-09-732-210-1367	Sequence 1367, Ap
9	41	48.8	212	4 US-10-140-002-482	Sequence 482, App
10	41	48.8	253	4 US-09-270-767-43223	Sequence 4322, A
11	41	48.8	4928	3 US-09-036-987A-5	Sequence 5, Appl1
12	41	48.8	4928	3 US-09-370-700-5	Sequence 5, Appl1
13	41	48.8	4928	4 US-09-603-807-5	Sequence 5, Appl1
14	40	47.6	151	4 US-09-732-210-1353	Sequence 1353, Ap
15	40	47.6	198	4 US-09-270-767-57545	Sequence 57545, A
16	40	47.6	356	4 US-09-270-767-42501	Sequence 42501, A
17	40	47.6	356	4 US-09-270-767-44479	Sequence 44479, A
18	40	47.6	356	4 US-09-270-767-44265	Sequence 44265, A
19	39.5	47.0	607	2 US-08-878-989-15	Sequence 15, Appl1
20	39.5	47.0	607	3 US-09-272-796-15	Sequence 15, Appl1
21	39	46.4	98	2 US-09-047-125-15	Sequence 15, Appl1
22	39	46.4	98	3 US-07-736-335E-15	Sequence 15, Appl1
23	39	46.4	189	4 US-09-710-279-1998	Sequence 1998, Ap
24	39	46.4	210	2 US-08-477-396A-18	Sequence 18, Appl1
25	39	46.4	210	4 US-09-270-767-45215	Sequence 45215, A
26	39	46.4	228	4 US-09-710-279-1166	Sequence 1166, Ap
27	39	46.4	265	4 US-09-248-796A-20923	Sequence 20923, A

28	39	46.4	286	3	US-09-134-001C-4103	Sequence 4103, Ap
29	39	46.4	382	4	US-09-266-965-104	Sequence 104, App
30	39	46.4	412	2	US-08-463-081B-14	Sequence 14, Appl1
31	39	46.4	412	2	US-08-461-379A-14	Sequence 14, Appl1
32	39	46.4	412	3	US-08-462-390B-14	Sequence 14, Appl1
33	39	46.4	412	2	US-08-463-074B-14	Sequence 14, Appl1
34	39	46.4	412	3	US-08-465-585C-14	Sequence 14, Appl1
35	39	46.4	412	3	US-08-652-446-14	Sequence 14, Appl1
36	39	46.4	412	3	US-09-462-624-2	Sequence 2, Appl1
37	38	45.2	87	4	US-09-270-767-41296	Sequence 41296, A
38	38	45.2	87	4	US-09-270-767-56512	Sequence 56512, A
39	38	45.2	168	4	US-09-252-991A-21932	Sequence 21932, A
40	38	45.2	190	4	US-09-252-991A-21938	Sequence 21938, A
41	38	45.2	207	4	US-09-328-352-6054	Sequence 6054, Ap
42	38	45.2	267	2	US-07-857-224B-42	Sequence 42, Appl1
43	38	45.2	553	4	US-09-252-991A-17984	Sequence 17984, A
44	38	45.2	842	4	US-09-489-039A-11570	Sequence 11570, A
45	38	45.2	1114	4	US-09-975-413A-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-08-310-340A-1
Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LKAMDPTPLMIKTE 15
Db 1 LKAMDPTPLMIKTE 15

RESULT 2

US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
SYNTHETIC LIPIDS AND THEIR
UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7280
TELEX:
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1

Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LKAMDPTPLMIKTE 15
Db 1 LKAMDPTPLMIKTE 15

RESULT 3

US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
SYNTHETIC LIPIDS AND THEIR
UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.029; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 LKAMDPTPL 10
DB 1 LKAMDPTPL 10

RESULT 4
US-08-188-582-20
Sequence 20, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanase, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLHR, HOHACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osaman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-582-20

Query Match 54.8%; Score 46; DB 1; Length 1213;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
DB 620 LSMDDSPVWIRLD 634

RESULT 5
US-08-646-715-20
Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanase, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLHR, HOHACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osaman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-715-20

Query Match 54.8%; Score 46; DB 1; Length 1213;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15

DB 620 LSAMDSPVLMIRLD 634

RESULT 6

US-09-134-000C-5938
Sequence 5938, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucelte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5938
LENGTH: 137
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5938

Query Match 53.6%; Score 45; DB 4; Length 137;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPLMT 12
:|||||:
Db 85 NPTPLMTV 92

RESULT 7

US-10-140-002-112
Sequence 112, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 112
LENGTH: 910
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-002-112

Query Match 50.0%; Score 42; DB 4; Length 910;
Best Local Similarity 46.7%; Pred. No. 2,1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMTKTE 15

DB 506 IECVDPTEPHNDTE 520

RESULT 8

US-09-732-210-1367
Sequence 1367, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Miltanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1367
LENGTH: 151
TYPE: PRT
ORGANISM: Zea mays
US-09-732-210-1367

Query Match 48.8%; Score 41; DB 4; Length 151;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPTPLMT 14
|||||:
Db 21 TPTPLMT 28

RESULT 9

US-10-140-002-482
Sequence 482, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 482
LENGTH: 212
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-002-482


```

; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PR1
; ORGANISM: Saccharopolyspora spinosa
US-09-603,207-5

```

Query Match	48.8%	Score 41	DB 4	Length 4928
Best Local Similarity	50.0%	Pred. No. 1.7e+03		
Matches	7	Conservative	3	Mismatches 4
				Indels 0
				Gaps 0

QY	1	LKAMDPTPLWIKT	14
		: : : :	
Db	2850	LRADVSAPLWLAT	2863

```

RESULT 14
US-09-732-210-1353
; Sequence 1353, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Ilang, Jihong
; APPLICANT: Miltanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(115036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; PRIORITY FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1353
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Agaricus bisporus
; US-09-732-210-1353

```

Query Match	47.6%	Score 40;	DB 4;	Length 151,
Best Local Similarity	75.0%;	Pred. No. 66;		
Matches	6;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;

```
QY      7 TPPLMIKT 14
        |||||:|
Db     21 TPPSWLKT 28
```

```

RESULT 15
US-09-270-767-57545
: Sequence 57545, Application US/09270767
: Patent No. 6703491
: GENERAL INFORMATION:
: APPLICANT: Homburger et al.
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US/09/270,767
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 57545
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
: FEATURE:
: OTHER INFORMATION: Xaa means any amino acid
: US-09-270-767-57545

```

Qy	1 LKADPTPLW 11	Best Local Similarity 54.5%	Pred. No. 88
	: : : :	Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0	
Db	70 IKAVSPSPNLW 80		

Search completed: January 6, 2005, 10:25:06
Job time : 31.4054 secs

Query Match 47.6%; Score 40; DB 4; Length 198;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2005, 10:09:21 ; Search time 18,8108 Seconds
(without alignments)
61.380 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDTPPLMT 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:***
2: PIR1:***
3: PIR2:***
4: PIR3:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	75.4	237	2	A42013	alpha-1-B-glycopro
2	43	62.3	695	2	E75099	hypothetical prote
3	43	62.3	932	1	A31898	hydroxymethylgluta
4	43	62.3	1213	2	A54063	TARA-binding prote
5	42	60.9	115	2	D71194	hypothetical prote
6	42	60.9	398	2	A81717	conserved hypothet
7	42	60.9	662	2	A29900	fasciclin I precur
8	42	60.9	1327	2	T09402	immunoglobulin-1lk
9	41	59.4	707	2	F86925	probable acyl-CoA
10	41	59.4	967	2	S58360	lanthibiotic Peps b
11	40	58.0	205	2	S26854	microfilariar sheat
12	40	58.0	205	2	A40525	proline-rich sheat
13	40	58.0	225	2	C70045	two-component resp
14	40	58.0	406	2	C83867	Xaa-Pro dipeptidas
15	40	58.0	560	2	T02404	probable beta-gluc
16	40	58.0	609	2	S65208	probable membrane
17	39.5	57.2	365	2	P87552	dpn protein [impo
18	39	56.5	268	2	S31010	gene 65 protein -
19	39	56.5	426	2	T16406	hypothetical prote
20	39	56.5	492	2	T16659	hypothetical prote
21	39	56.5	564	1	VHXPMV	major structural n
22	39	56.5	564	1	A69798	beta-galactosidase
23	39	56.5	1212	2	D88175	protein T24H7.5a l
24	39	56.5	1215	2	E70614	hypothetical prote
25	39	56.5	1454	2	C88175	protein T24H7.5b l
26	39	56.5	1728	2	T17466	riifamycin polyketi
27	38.5	55.8	401	1	REMSK	renin (EC 3.4.23.1
28	38.5	55.8	402	1	REMSK	renin (EC 3.4.23.1
29	38	55.1	259	2	C71820	hypothetical prote

30	38	55.1	347	2	B70710	hypothetical prote
31	38	55.1	364	2	T10945	peroxidase (EC 1.1
32	38	55.1	660	2	T22794	hypothetical prote
33	38	55.1	792	2	T29187	hypothetical prote
34	38	55.1	896	2	C85438	hypothetical prote
35	38	55.1	1127	2	B97580	hypothetical prote
36	38	55.1	1325	2	S62497	probable nucleopor
37	38	55.1	1443	2	S05979	steroid hormone re
38	37.5	54.3	1145	2	T33606	hypothetical prote
39	37	53.6	86	2	AB2368	hypothetical prote
40	37	53.6	116	2	G72520	hypothetical prote
41	37	53.6	142	2	AB1681	similar o transcri
42	37	53.6	144	2	AG2568	hypothetical prote
43	37	53.6	149	2	AB3045	hypothetical prote
44	37	53.6	162	2	C70829	hypothetical prote
45	37	53.6	212	2	C87585	hypothetical prote

ALIGNMENTS

RESULT 1
A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C/Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossi
C/Date: 10-Jul-1992 #sequence_rev1sion 10-Jul-1992 #text_change 09-Jul-2004
C/Accession: A42013
R/Catane, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A/Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hu
A/Reference number: A42013; PMID:92118934; PMID:1731898
A/Accession: A42013
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-237 <CAT>
C/Cross-references: UNIPROT:Q28359; GB:J05356
C/Keywords: glycoprotein

Query Match 75.4%; Score 52; DB 2; Length 237;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDTPPLMT 12
DB 1 LKAMDTPPLMT 12

RESULT 2
E75099
hypothetical protein PAB1590 - Pyrococcus abyssi (strain Ozeay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_rev1sion 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: E75099
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A/Reference number: A75001
A/Accession: E75099
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-695 <RAW>
A/Cross-references: UNIPROT:Q9U2G1; GB:AJ248286; GB:AL096836; NID:95458366; PIDN:CB500
C/Experimental source: strain Ozeay
C/Genetics:
A/Genes: PAB1590

Query Match 62.3%; Score 43; DB 2; Length 695;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPLMT 12
DB 561 ANDKPRMTL 570

RESULT 3

A11898
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrotus purpuratus)

C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A31898; A28367
R/Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.

J. Biol. Chem. 263, 18411-18419, 1988

A/Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduced from complementary DNA

A/Reference number: A31898; MUID:89054023; PMID:3192541

A/Accession: A31898

A/Molecule type: mRNA

A/Residues: 1-932 <WOO>

A/Cross-references: UNIPROT:P16393; GB:J04200; NID:9161522; PIDN:AAA30060.1; PID:9161523

A/Note: the authors rearranged portions of the coding region in Figure 2, and the above submitted to GenBank

A/Note: the authors translated the codon GGA for residue 805 as Glu

R/Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.

J. Biol. Chem. 263, 2513-2517, 1988

A/Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev

A/Reference number: A28367; MUID:88115403; PMID:3276692

A/Accession: A28367

A/Molecule type: mRNA

A/Residues: 689-735 <WOO>

C/Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in the biosynthesis of cholesterol

C/Suprafamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase

C/Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N

F/279,850,886,930/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 62.3%; Score 43; DB 1; Length 932; Best Local Similarity 70.0%; Pred. No. 38; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPLM 11
| : ||| |||
DB 298 KKDPTPLM 307

RESULT 4

A54063
TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: A54063
R/Vierjzen, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.

Science 264, 933-941, 1994

A/Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to C

A/Reference number: A54063; MUID:94233377; PMID:8176153

A/Accession: A54063

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1213 <YER>

A/Cross-references: UNIPROT:Q24325; GB:X79243; NID:9541664; PIDN:CAAS5830.1; PID:9541665

A/Genetic: FlyBase:Tafl50

A/Genetic: FlyBase:Tafl50

A/Cross-references: FlyBase:Tafl50

Query Match 62.3%; Score 43; DB 2; Length 1213; Best Local Similarity 66.7%; Pred. No. 52; Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 12
| : ||| |||
DB 620 LKAMDPTPLM 631

RESULT 5

D71194
hypothetical protein PH1828 - Pyrococcus horikoshii

C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C/Accession: D71194

R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A/Reference number: A71000; MUID:98344137; PMID:9679194

A/Accession: D71194

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-115 <KAM>

A/Cross-references: UNIPROT:O59492; GB:A000007; NID:93236134; PIDN:BA30947.1; PID:9325

A/Experimental source: Strain OT3

A/Note: this accession replaces an interim accession for a sequence replaced by GenBank

C/Genetics: PH1828

Query Match 60.9%; Score 42; DB 2; Length 115; Best Local Similarity 66.7%; Pred. No. 5.5; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPPTPLM 12
| : ||| |||
DB 89 ISPPPLM 97

RESULT 6

A81717
conserved hypothetical protein TC0306 (imported) - Chlamydia muridarum (strain N19g)

C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: A81717
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: A81717

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-398 <TEP>

A/Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:97190343; PIDN:AAF3917

A/Experimental source: Strain N19g (MoPn)

C/Genetics: TC0306

C/Suprafamily: Chlamydia trachomatis hypothetical protein TC036

Query Match 60.9%; Score 42; DB 2; Length 398; Best Local Similarity 77.8%; Pred. No. 22; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
| : ||| |||
DB 309 KKDPTPL 317

RESULT 7

A29900
fasciclin I precursor - American bird grasshopper

C/Species: Schistocerca americana (American bird grasshopper)
C/Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 09-Jul-2004

C/Accession: A29900; A31817
R/Zinn, K.; McAllister, L.; Goodman, C.S.

Cell 53, 577-587, 1988

A/Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Dro

A/Reference number: A29900; MUID:88223351; PMID:3370670

A/Accession: A29900

A/Molecule type: mRNA

A/Residues: 1-662 <ZIN>

A/Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:9160846; PID:9160847

R/Smith, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Baetian, M.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988

A/Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t

A:Reference number: A94202; MUID:88276943; PMID:2839842

A:Accession: A31817

A:Molecule type: mRNA

A:Residues: 25-42 <SNO>

A:Cross-references: EMBL:M20544; EMBL:J03787

Query Match 60.9%; Score 42; DB 2; Length 662;

Best Local Similarity 58.3%; Pred. No. 39;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM1 12

DB 104 LSELDPNPLM1 115

RESULT 8

T09402

Immunoglobulin-like protein IGSF1 - human

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09402

R:Maszarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.

Genomics 48, 157-162, 1998

A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.

A:Reference number: Z1665; MUID:98190514; PMID:9521868

A:Accession: T09402

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1327 <MAZ>

A:Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AC52057.1; PID:g2

A:Gene: igsf1

A:Map position: Xq25

Query Match

Best Local Similarity 77.8%; Score 42; DB 2; Length 1327;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPPTPLM1 12

DB 25 MDPQPLM1 33

RESULT 9

P86925

Probable acyl-CoA synthetase [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: P86925

R:Coile, S.T.; Eglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Dutroy, S.; Feltwell, T.; Frazer, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: P86925

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-707 <STO>

A:Cross-references: UNIPROT:Q9CD82; GB:AL450380; NID:g13092512; PIDN:CA629642.1; GSPDB:C

C:Gene: ladd22

A:Gene: ladd22

Query Match

Best Local Similarity 59.4%; Score 41; DB 2; Length 707;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM1 11

DB 486 LRAQSPKPIW 496

RESULT 10

S58360

Antibiotic Pept biosynthesis protein pept - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S58360

R:Meier, C.; Bierbaum, G.; Heldrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Keu

Eur. J. Biochem. 232, 478-489, 1995

A:Title: Nucleotide sequence of the antibiotic Pept biosynthetic gene cluster and funci

A:Reference number: S56551; MUID:96035882; PMID:7556197

A:Accession: S56555

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-967 <ME2>

A:Cross-references: UNIPROT:Q54123; EMBL:Z49865; NID:g945014; PIDN:CAA90025.1; PID:g945

C:Gene: pept

A:Keywords: antibiotic biosynthesis

Query Match

Best Local Similarity 59.4%; Score 41; DB 2; Length 967;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM1 11

DB 102 LKAMDPTPLM1 112

RESULT 11

S26854

microfilament sheath protein, major component - nematode (Brugia pahangi)

C:Species: Brugia pahangi

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S26854

R:Selkirk, M.

Submitted to the EMBL Data Library, February 1991

A:Reference number: S26854

A:Accession: S26854

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-205 <SEL>

A:Cross-references: UNIPROT:Q00032; EMBL:X58063; NID:g5951; PID:g5952

C:Gene: h23/2

A:Introns: 123/2

Query Match

Best Local Similarity 58.0%; Score 40; DB 2; Length 205;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM1 11

DB 146 LTOQRTPLM1 156

RESULT 12

A40525

proline-rich sheath protein ME22 precursor - nematode (Brugia pahangi)

C:Species: Brugia pahangi

C>Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004

C:Accession: A40525; S18744

R:Belkirk, M.B.; Yazdanhahsh, M.; Freedman, D.; Blaxter, M.L.; Cookson, B.; Jenkins, R

J. Biol. Chem. 266, 11002-11008, 1991

A:Title: A proline-rich structural protein of the surface sheath of larval Brugia filar

A:Reference number: A40525; MUID:91550404; PMID:1710216

A:Accession: A40525

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-205 <SEL>

A:Cross-references: UNIPROT:Q00032; GB:X58063

A:Note: the authors translated the codon GCA for residue 23 as Arg, CUG for residue 146

Query Match

Best Local Similarity 58.0%; Score 40; DB 2; Length 205;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM1 11

DB 486 LRAQSPKPIW 496

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 LKAMDPTPLM 11
|:|||||:
DB 146 LTKQOTPTPTM 156

RESULT 13

C70045

two-component response regulator [YvqB] homolog yvqA - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: C70045

R/Kunitz, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet

C.; Bron, S.; Brouillette, S.; Brunsch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho

A.; Enllich, S.D.; Emerson, P.T.; Enlian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizai, A.; Gall

lech, U.; Harwood, C.R.; Hentz, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogizawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelid

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon

A/Authors: Schleich, S.; Schroeder, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akuch, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:96044033; PMID:9364377

A/Accession: C70045

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-225 <KUN>

A/Cross-references: UNIPROT:O32192; GB:Z99120; GB:AL009126; NID:G2635613; PIDN:CAM15291.

A/Experimental source: strain 168

C/Genetics:

A/Genes: yvqA

C/Superfamily: ompR protein; response regulator homology

C/Keywords: phosphoprotein

F.5.113/Domain: response regulator homology <RRH>

F.52/Binding site: phosphate (asp) (covalent) #status predicted

Query Match 58.0%; Score 40; DB 2; Length 225;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLM 12
|:|||||:
DB 40 KKMTPSPHLM 50

RESULT 14

C83867

Xaa-Pro dipeptidase BH1739 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: C83867

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: C83867

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-406 <STO>

A/Cross-references: UNIPROT:Q9KC35; GB:AP001513; GB:BA000004; NID:G10174345; PIDN:BA054

A/Experimental source: strain C-125

C/Genetics:

A/Genes: BH1739

Query Match 58.0%; Score 40; DB 2; Length 406;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPLM 12
|:|||||:
DB 369 PSPPLMV 395

RESULT 15

T02404

probable beta-glucosidase homolog P411.30 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C/Accession: T02404; B84879

R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, May 1998

A/Description: Arabidopsis thaliana chromosome II BAC P411 genomic sequence.

A/Reference number: Z14667

A/Accession: T02404

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-560 <ROU>

A/Cross-references: UNIPROT:O64883; EMBL:AC004521; NID:G3128166; PIDN:ACC16095.1; PID:G3

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Bentol, M.L.; Town, C.D.; Fujii, C.Y.;

W.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, L.; Tallon, L

euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: B84879

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-560 <STO>

A/Cross-references: GB:AE002093; NID:G3128191; PIDN:ACC16095.1; GSPDB:GN00139

C/Genetics:

A/Genes: At3g4490; P411.30

A/Map position: 2

A/Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2

C/Superfamily: Agrobacterium beta-glucosidase

Query Match 58.0%; Score 40; DB 2; Length 560;
Best Local Similarity 54.5%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
|:|||||:
DB 334 IKHVDPTQPTM 344

Search completed: January 6, 2005, 10:23:50
Job time : 20.8108 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:00:35 ; Search time 102.811 Seconds
(without alignments)
67.157 Million cell updates/sec

Title: US-10-047-945-4
Perfect score: 69
Sequence: 1 LKAMDPTPLMI 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	17	09TR78	09TR78 didelphis m
2	69	100.0	291	DM43_DIDMR	P82957 didelphis m
3	60	87.0	140	08HZ75	08HZ75 didelphis m
4	60	87.0	291	08HZ74	08HZ74 didelphis m
5	52	75.4	314	08HYX5	08HYX5 didelphis m
6	50	72.5	227	073ZB2	073ZB2 mycobacteri
7	50	72.5	227	AAS04008	AAS04008 mycobacteri
8	46	66.7	370	07OR48	07OR48 anophelis g
9	45	65.2	128	0833V1	0833V1 anophelis g
10	45	65.2	467	07YQV7	07YQV7 sus. scrofa
11	44	63.8	242	08BXK6	08BXK6 mus musculu
12	44	63.8	477	018150	018150 caenorhabdt
13	43	62.3	351	Y4VU RHLSN	053218 rhizobium s
14	43	62.3	354	08VM74	08VM74 rhizobium s
15	43	62.3	360	0846T8	0846T8 myxococcus
16	43	62.3	695	09UZG1	09UZG1 pyrococcus
17	43	62.3	932	HMDH_STRPU	P16333 streptococ
18	43	62.3	1221	TAF2_DROME	024355 drosophila
19	42	60.9	115	059492	059492 pyrococcus
20	42	60.9	190	07Q3Z4	07Q3Z4 anophelis g
21	42	60.9	242	08N6C5	08N6C5 homo sapien
22	42	60.9	356	06FB99	06FB99 acinetobact
23	42	60.9	398	Y306_CHLMU	09P102 chlamydia m
24	42	60.9	408	07WLE6	07WLE6 bordetella
25	42	60.9	576	06YID6	06YID6 penaeus mon
26	42	60.9	576	AAN17670	AAN17670 penaeus mon
27	42	60.9	612	083WV7	083WV7 streptococ
28	42	60.9	662	FAS1_SCHAM	P15070 schistosom
29	42	60.9	1437	015070	015070 homo sapien
30	41	59.4	51	08FND0	08FND0 corynebacte
31	41	59.4	99	06CS47	06CS47 kluyveriomyc

32	41	59.4	125	2	09NV61	09NV61 homo sapien
33	41	59.4	165	2	09W3H5	09W3H5 drosophila
34	41	59.4	212	2	06UM07	06UM07 homo sapien
35	41	59.4	212	2	AAG89419	AAG89419 homo sapi
36	41	59.4	222	2	09HBJ8	09HBJ8 homo sapien
37	41	59.4	344	2	07MTQ9	07MTQ9 porphyromon
38	41	59.4	504	2	08MTS3	08MTS3 didelphis m
39	41	59.4	634	2	09VOP3	09VOP3 drosophila
40	41	59.4	707	2	09CD82	09CD82 mycobacteri
41	41	59.4	854	2	09VQP4	09VQP4 drosophila
42	41	59.4	856	2	09G210	09G210 drosophila
43	41	59.4	967	2	054123	054123 staphylococ
44	41	59.4	1017	2	07KJ30	07KJ30 drosophila
45	41	59.4	1017	2	AAS64617	AAS64617 drosophila

ALIGNMENTS

```

RESULT 1
ID 09TR78      PRELIMINARY;      PRT;      17 AA.
AC 09TR78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTHRORPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694;
RA Perales J., Mousatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-botrophic complex
RT from the serum of South American didelphidae.";
RL Toxicol 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MM; CBS5FB40E73B2A2A CRC64;

Query Match      100.0%; Score 69; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMDPTPLMI 12
      |||||
Db      1 LKAMDPTPLMI 12

RESULT 2
ID DM43_DIDMR      STANDARD;      PRT;      291 AA.
AC P82957;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RX MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.;
RA Makino D.L., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
RT metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -I- FUNCTION: Metalloproteinase inhibitor.
CC -I- SUBUNIT: Homodimer.
CC -I- TISSUE SPECIFICITY: Blood and milk.

```

CC -1- PTM: N-glycosylated.
 CC -1- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR011015; IEM_like.
 DR Pfam; PF00047; Ig, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KM Metalloprotease inhibitor; Repeat.
 FT DOMAIN 22 79 Ig-like V-type 1.
 FT DOMAIN 114 171 Ig-like V-type 2.
 FT DOMAIN 191 288 Ig-like V-type 3.
 FT DISULFID 28 74 Potential.
 FT DISULFID 121 163
 FT DISULFID 213 265
 FT CARBOHYD 23 23 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 156 156 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 160 160 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 175 175 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 291 AA; 32390 MW; 17A496227B69A65B CRC64;

Query Match 100.0%; Score 69; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMI 12
 Db 1 LKAMDPTPLMI 12

RESULT 3
 Q8H275 PRELIMINARY; PRT; 140 AA.

AC Q8H275; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 26, Last annotation update)
 DE Alpha 1B glycoprotein DVOP1-D (Fragment).
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Martinez M.E., Pierce J.R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY131000; AAN06911.1;
 DR InterPro; IPR011015; IEM_like.
 FT NON_TER 1
 FT NON_TER 140
 SQ SEQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

Query Match 87.0%; Score 60; DB 2; Length 140;
 Best Local Similarity 91.7%; Pred. No. 0.075;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMI 12
 Db 42 LKAMDPTPLMI 53

RESULT 4
 Q8H274 PRELIMINARY; PRT; 291 AA.

AC Q8H274; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 26, Last annotation update)
 DE Alpha 1B glycoprotein DVOP14 (Fragment).
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Martinez M.E., Pierce J.R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY131001; AAN06912.1;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR011015; IEM_like.
 DR Pfam; PF00047; Ig, 1.
 DR SMART; SM00409; IG, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 291
 SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;

Query Match 87.0%; Score 60; DB 2; Length 291;
 Best Local Similarity 91.7%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMI 12
 Db 1 LKAMDPTPLMI 12

RESULT 5
 Q8H275 PRELIMINARY; PRT; 314 AA.

AC Q8H275; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 26, Last annotation update)
 DE Venom metalloprotease inhibitor DW43b precursor.
 OS Didelphis marsupialis (Southern opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9268;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Tringilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C.,
 RA Domont G.B., Ho P.L., Perales J.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY163806; AAN64698.1;
 DR InterPro; IPR003599; IG_LIKE.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig, 1.
 DR SMART; SM00409; IG, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal.
 FT SIGNAL 1
 FT CHAIN 24 23 Potential.
 SQ SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 314;
 Best Local Similarity 83.3%; Pred. No. 3.5;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLMI 12
 Db 24 LKAMDPTPLMI 35

RESULT 6
 Q732B2 PRELIMINARY; PRT; 227 AA.

AC Q732B2; (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MAP1691c;

```

OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K10;
RA Li U., Bannantine J., Zhang Q., Ammons A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017233; AAS04008.1; -
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;

Query Match 72.5%; Score 50; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
DB 146 LAALDPTPLM 156

RESULT 7
AAS04008 PRELIMINARY; PRT; 227 AA.
AC AAS04008;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN MAP1691C.
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K10;
RA Li U., Bannantine J., Zhang Q., Ammons A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017233; AAS04008.1; -
KM Hypothetical protein.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;

Query Match 72.5%; Score 50; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
DB 146 LAALDPTPLM 156

RESULT 8
Q70E48 PRELIMINARY; PRT; 370 AA.
AC Q70E48;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE AgCP225 (Fragment).
GN Name=agCG51396; ORFNames=ENSG000000014288;
OS Anopheles gambiae str. PEST.
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Contains 2 C2 domains.

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CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100848; BAA07048.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006101; F:transport; IEA.
DR InterPro; IPR002149; Alatroxin_recept.
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PROSITE; PSS0004; C2_DOMAIN_2; 2.
PT NON_TER
SQ SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8DF CRC64;

Query Match 66.7%; Score 46; DB 2; Length 370;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
DB 294 IRALDPTPLM 304

RESULT 9
Q833V1 PRELIMINARY; PRT; 128 AA.
AC Q833V1;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Conserved domain protein.
GN OrderedLocNames=EF1825;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=2250857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.B., Seshadri R.,
RA Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F.,
RA Tectelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouli H.M., Uettersack T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074(2003).
DR EMBL; AB016952; AAO81592.1; -
DR TIGR; EF1825; -
KM Complete proteome.
SQ SEQUENCE 128 AA; 14458 MW; 43459A9BE814572F CRC64;

Query Match 65.2%; Score 45; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPLM 12
DB 76 NPTPLM 83

RESULT 10
Q7YQJ7 PRELIMINARY; PRT; 467 AA.
AC Q7YQJ7;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Organic anion transporter OATF1.

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GN Name=catyl;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Apical membrane of renal proximal tubule in kidney cortex;
RX MEDLINE=22753825; PubMed=12740363;
RA Jutaba P., Kanai Y., Hosoyamada M., Chairoungkhua A., Kim D.K.,
RA Iribe Y., Babu E., Kim J.Y., Anzal N., Chaturuthipong V., Endou H.,
RT Identification of a novel voltage-driven organic anion transporter
RT present at apical membrane of renal proximal tubule."
RL J. Biol. Chem. 278:27930-27938 (2003).
DR EMBL; AB104465; BAC76761.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
SQ SEQUENCE 467 AA; 52069 MW; 2B065005C3FDCAB6 CRC64;

Query Match 65.2%; Score 45; DB 2; Length 467;
Best Local Similarity 58.3%; Pred. No. 74;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LKAMPPTPLW1 12
DB 255 IKAMIKSPLMV 266

RESULT 11
Q8BXK6 PRELIMINARY; PRT; 242 AA.
AC O8BXK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
DE library, clone:330018M03 product:hypothetical fibronectin type III
DE structure containing protein, full insert sequence.
GN Name=B930041F14R1K;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitanaka T., Tashiro H., Itoh M.,
RA Sun H., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK046537; BAC32775.1; -
DR MGP; MGI:2444790; B930041F14R1K.
DR Hypothetical protein.
KW SEQUENCE 242 AA; 26120 MW; FD8FE24EB994F8F0 CRC64;
SQ

Query Match 63.8%; Score 44; DB 2; Length 242;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AMDPTPLW1 11
DB 20 AVDPTPGW 28

RESULT 12
Q18150 PRELIMINARY; PRT; 477 AA.
AC Q18150;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nuclear hormone receptor family protein 120.
GN Name=nhr-120; ORFNames=C25B8.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

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RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRIE101 N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRIE101 N2;
 RA Wilson R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRIE101 N2;
 RA Wilson R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC EMBL; U41556; AK39191.2; -.
 DR HSSP; P20393; 1A6Y.
 DR WormDep; C25B8.6; CE30877.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003707; P:steroid hormone receptor activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000536; Hrmom_recept_1lg.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR000324; Vldf_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STROIDPINGER.
 DR PRINTS; PR00350; VITAMINDR.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor;
 KM Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 477 AA; 54900 MW; 9D168F3BDC0241 CRC64;
 Query Match 63.8%; Score 44; DB 2; Length 477;
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KANDPTPLMI 12
 DB 18 KLAHPSPPMWI 28
 RESULT 13
 Y4VJ_RHISN STANDARD; PRT; 351 AA.
 ID Y4VJ_RHISN
 AC 053218;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical 39.2 kDa protein y4vJ.
 GN OREName=y4vJ;
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym PNGR234.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NC NCB1_taxid=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes";
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE OF 1-279 FROM N.A.
 RX MEDLINE=96389014; PubMed=8796346;
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;

RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
 RT NGR234 using dye terminators and a thermostable 'sequenase': a
 RT beginning.";
 RL Genome Res. 6:590-600(1996).
 CC -1- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; Z68203; CAA92425.1; -.
 DR EMBL; A5000101; AAB91898.1; -.
 DR InterPro; IPR002103; Bac_luciferase.
 DR InterPro; IPR011251; Luciferase_like.
 DR Pfam; PF00296; Bac_luciferase; 1.
 KW Hypothetical protein; Monooxygenase; Oxidoreductase; Plasmid.
 SQ SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C8D CRC64;
 Query Match 62.3%; Score 43; DB 1; Length 351;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PTPPLMI 12
 DB 167 PTPPLMI 173
 RESULT 14
 Q8VW74 PRELIMINARY; PRT; 354 AA.
 ID Q8VW74
 AC 08VW74;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative LuxA.
 OS Rhizobium sp. (strain BR816).
 OG Plasmid pSymA.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NC NCB1_taxid=48291;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BR816;
 RL Luyten E., Verreth C., Vanderleyden J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BR816;
 RA Luyten E., Swinnen E., Verreth C., Vlassak K., Dombrecht B.,
 RA Vanderleyden J.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U26451; AAL61964.1; -.
 DR EMBL; U26451; AAL61964.1; -.
 DR InterPro; IPR002103; Bac_luciferase.
 DR InterPro; IPR011251; Luciferase_like.
 DR Pfam; PF00296; Bac_luciferase; 1.
 KW Plasmid.
 SQ SEQUENCE 354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;
 Query Match 62.3%; Score 43; DB 2; Length 354;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PTPPLMI 12
 DB 167 PTPPLMI 173
 RESULT 15

Q846T8
 ID O846T8 PRELIMINARY; PRT; 360 AA.
 AC O846T8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical adventurous gliding motility protein M.
 GN Name=agmM;
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cystobacterineae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hartzell P.L., Youderian P.A.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -|- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -|- SIMILARITY: Belongs to peptidase family M48.
 CC EMBL; AY197568; AAC6299.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004322; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001915; Peptidase_M48.
 DR Pfam; PF01435; Peptidase_M48; 1.
 KW Hydrolase; Hypothetical protein; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 360 AA; 40304 MW; 98AB27E93EAE023 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 360;
 Best Local Similarity 66.7%; Fred. NO. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 MDPPTPLMI 12
 Db 332 MDPEPRRW 340

Search completed: January 6, 2005, 10:17:48
 Job time : 104.811 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:08:37 ; Search time 95.3513 Seconds
(without alignment)

45.146 Million cell updates/sec

Title: US-10-047-945-4

Sequence: 1 KAMDPTPLMT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq238ep04:*

1: _geneseqp1980s:*\n2: _geneseqp1980s:*\n3: _geneseqp2000s:*\n4: _geneseqp2001s:*\n5: _geneseqp2002s:*\n6: _geneseqp2003as:*\n7: _geneseqp2003bs:*\n8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	12	7	ABBB0225 Synthetic
2	69	100.0	15	2	AAW11575 N-termina
3	69	100.0	15	2	AAW53841 N-termina
4	69	100.0	15	7	ABBB0223 Synthetic
5	65	94.2	11	7	ABBB0226 Synthetic
6	54	78.3	10	2	AAW53843 N-terminu
7	54	78.3	10	7	ABBB0222 Synthetic
8	50	72.5	9	7	ABBB0227 Synthetic
9	45	65.2	137	7	ADH88053 Enterococ
10	44	63.8	156	4	ABG22890 Novel hum
11	44	63.8	303	4	ABG18144 Novel hum
12	43	62.3	8	7	ABBB0228 Synthetic
13	43	62.3	393	8	AAW79784 Human pro
14	43	62.3	932	8	ADM98800 HMG-CoA t
15	43	62.3	1189	2	AAW56496 TATA-bind
16	43	62.3	1213	2	AAW06086 Drosophila
17	43	62.3	1213	2	AAW25029 TATA-bind
18	43	62.3	1219	4	ABBB6218 Drosophila
19	42	60.9	94	4	AAW02179 Human pol
20	42	60.9	242	7	ADB80591 Human pit
21	42	60.9	299	7	ADB90617 Human pit
22	42	60.9	612	8	ADH39800 Streptomy
23	42	60.9	1336	6	ABR47496 Breast ca
24	42	60.9	1336	8	ADP18673 Human pro
25	42	60.9	1457	4	AAU32796 Novel hum

ALIGNMENTS

25	41	59.4	9	6	ABR12621	Abri12621 Human can
27	41	59.4	9	6	ABR12017	Abri12017 Human can
28	41	59.4	9	6	ABR12854	Abri12854 Human can
29	41	59.4	10	6	ABR12743	Abri12743 Human can
30	41	59.4	10	6	ABR11875	Abri11875 Human can
31	41	59.4	10	6	ABR12121	Abri12121 Human can
32	41	59.4	10	6	ABR12948	Abri12948 Human can
33	41	59.4	10	6	ABR12106	Abri12106 Human can
34	41	59.4	10	6	ABR12294	Abri12294 Human can
35	41	59.4	10	6	ABR12738	Abri12738 Human can
36	41	59.4	15	6	ABR33125	Abri33125 Human can
37	41	59.4	15	6	ABR33383	Abri33383 Human can
38	41	59.4	15	6	ABR33116	Abri33116 Human can
39	41	59.4	15	6	ABR33427	Abri33427 Human can
40	41	59.4	15	6	ABR33563	Abri33563 Human can
41	41	59.4	17	4	ABR42105	Abri42105 Peptide #
42	41	59.4	37	4	AAW5798	AAW5798 Human bra
43	41	59.4	37	4	AAW62985	AAW62985 Human bra
44	41	59.4	64	4	ABR40295	ABR40295 Peptide #
45	41	59.4	64	4	AAW33978	AAW33978 Peptide #

RESULT 1
ID ABB80225 standard; peptide; 12 AA.

AC ABB80225;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNF, LT-12.

KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B;

KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;

KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;

KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;

KW Graves' disease; Addison's disease; Hodgkin's disease; depression;

KW saliva; ELISA.

OS Synthetic.

PN WO2003060471-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPE/) LIIPS B V.

PA (LIPE/) LIIPS F W.

PT Lippe BV, Lippe FW;

PT WPI; 2003-636703/60.

PS Assaying a human endogenous protein (e.g. IGE, nerve growth factor,

PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.

PT asthma or diabetes, by employing an ELISA on a saliva sample from a

CC patient.

CC Claim 7; Page 4; 24p; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising

CC factor (LTNP) peptides which may be used for reducing elevated levels of

CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor

CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In

CC particular, the methods of the invention are useful for diagnosing and

CC treating conditions with elevated serum IGE levels, e.g. asthma,

CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 69; DB 7; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 12
 DB 1 LKAMDPTPLMT 12

RESULT 2
 AAW1575
 ID AAW1575 standard; peptide; 15 AA.

XX AC AAW1575;

DT 25-MAR-2003 (revised)
 DT 20-MAR-1997 (first entry)

XX DE N-terminal peptide from lethal toxin neutralising factor.

XX KW Lethal toxin neutralising factor; LTNP; opoosum; bee toxin;
 XX scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX OS Didelphis virginiana.

XX PN US5576297-A.

XX PD 19-NOV-1996.

XX PF 22-SEP-1994; 94US-00310340.

XX PR 10-MAY-1993; 93US-00058387.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1997-011287/01.

XX PT Treatment of victims of bee or scorpion stings or plant or bacterial
 XX PT toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
 XX PT peptide.

XX PS Claim 7; Col 9; 9pp; English.

XX CC The present sequence is from the N-terminus of a 68 kD protein purified
 XX CC from the serum of the opossum *Didelphis virginiana*. The full-length
 XX CC protein is a lethal toxin neutralising factor (LTNP). The use of purified
 XX CC LTNP or of the chemically synthesised 15mer N-terminal peptide for
 XX CC treating victims of bee stings, scorpion stings and bacterial or plant
 XX CC toxins is claimed. The patent disclosure does not provide any evidence
 XX CC for neutralising activity against these various toxins. There is evidence
 XX CC of significant neutralising activity of the opossum LTNP and the 15mer
 XX CC peptide against venom from snakes of the families Crotalidae, Elapidae,
 XX CC Hydroiidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 69; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 12
 DB 1 LKAMDPTPLMT 12

RESULT 3
 AAW53841
 ID AAW53841 standard; peptide; 15 AA.

XX AC AAW53841;

DT 08-JUL-1998 (first entry)

XX DE N-terminus of opoosum LTNP.

XX KW LTNP; lethal toxin neutralising factor; opoosum; envenomation; therapy;
 XX KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 XX KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 XX KW histamine reaction treatment.

XX OS Didelphis virginiana.

XX PN US5744449-A.

XX PD 28-APR-1998.

XX PE 03-JUN-1996; 96US-00657163.

XX PR 10-MAY-1993; 93US-00058387.

XX PR 22-SEP-1994; 94US-00310340.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1998-271108/24.

XX PT Lethal Toxin Neutralising Factor peptide from opoosum - can neutralise
 XX PT venom(s) from all major families of poisonous snakes.

XX PS Claim 1; Col 11; 11pp; English.

XX CC This sequence represents the peptide of the invention. It is a lethal
 XX CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 XX CC protein derived from an opoosum. The peptide can be used in a method for
 XX CC treating a victim of envenomation from a poisonous snake, preferably a
 XX CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 XX CC is useful for the treatment of snake bites, sepsis, allergies caused by
 XX CC the environment and treatment of bee or scorpion stings or toxicities
 XX CC caused by plant or bacterial toxins. The peptide can also be used in
 XX CC histamine reaction treatment. The peptide can be used in envenomation
 XX CC treatment for a variety of snakes without prior identification of the
 XX CC snake. Being short it can be synthetically prepared rather than the
 XX CC current production in horses, where some people can show hypersensitivity
 XX CC to horse proteins

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 69; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 12
 DB 1 LKAMDPTPLMT 12

RESULT 4
 ABB80223

ID	ABB80223 standard; peptide; 15 AA.
AC	ABB80223;
DT	06-NOV-2003 (first entry)
DE	Synthetic LTNP, LT-15.
KW	Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
OS	Synthetic.
PN	WO2003060471-A2.
PD	24-JUL-2003.
PF	14-JAN-2003; 2003WO-US001044.
PR	14-JAN-2002; 2002US-00047945.
XX	(LIPP/) LIPPS B V.
PA	(LIPP/) LIPPS F W.
P1	Lipps BV, Lipps FW;
XX	WPI, 2003-636703/60.
XX	Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT	insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT	asthma or diabetes, by employing an ELISA on a saliva sample from a
XX	patient.
XX	Claim 3; Page 3; 24pp; English.
XX	The sequences given in ABB80222-28 represent lethal toxin neutralising
CC	factor (LTNP) peptides which may be used for reducing elevated levels of
CC	serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC	(NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC	particular, the methods of the invention are useful for diagnosing and
CC	treating conditions with elevated serum IgE levels, e.g. asthma,
CC	diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC	arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC	Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC	the protein may be monitored by assaying a human endogenous protein by
CC	performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC	sample using an anti-serum that is specific for the protein. Saliva
CC	collection is relatively non-invasive when compared to blood collection
CC	for serum. Saliva can be centrifuged immediately, whereas blood requires
CC	clotting time before centrifugation to separate serum. Saliva proteins
CC	can be assayed by a simple ELISA test, whereas an assay of proteins from
CC	serum requires a more complicated sandwich type ELISA
XX	
XX	Sequence 15 AA;
XX	
QY	Query Match 100.0%; Score 69; DB 7; Length 15;
D8	Best Local Similarity 100.0%; Pred. NO. 0.00039;
DB	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 LKANDPTPLWT 12
	1 LKANDPTPLWT 12
RESULT 5	
ABB80226	
ID	ABB80226 standard; peptide; 11 AA.
AC	ABB80226;

XX	06-NOV-2003	(first entry)
DT		
XX	Synthetic LTNP, LT-11.	
XX		
XX	Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;	
KW	IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;	
KW	ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;	
KW	SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;	
KW	Graves' disease; Addison's disease; Hodgkin's disease; depression;	
KW	saliva; ELISA.	
XX		
OS	Synthetic.	
XX		
FN	WO2003060471-A2.	
PD		
PD	24-JUL-2003.	
XX		
PE	14-JAN-2003; 2003WO-US001044.	
XX		
XX	14-JAN-2002; 2002US-00047945.	
XX		
PA	(LIPP/) LIPPS B V.	
XX	(LIPP/) LIPPS F W.	
PL	Lipps BV, Lipps FW;	
DR	WPI; 2003-636703/60.	
PT		
PT	Assaying a human endogenous protein (e.g. IGF, nerve growth factor,	
PT	insulin or diabetes, by employing an ELISA on a saliva sample from a	
PT	patient.	
XX		
PS	Claim 7; Page 4; 24pp; English.	
XX		
CC	The sequences given in ABB80222-28 represent lethal toxin neutralising	
CC	factor (LTNP) peptides which may be used for reducing elevated levels of	
CC	serum proteins selected from immunoglobulin E (IgE), nerve growth factor	
CC	(NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In	
CC	particular, the methods of the invention are useful for diagnosing and	
CC	treating conditions with elevated serum IGF levels, e.g. asthma,	
CC	diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid	
CC	arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,	
CC	Addison's disease or Hodgkin's disease) or depression. The efficacy of	
CC	the protein may be monitored by assaying a human endogenous protein by	
CC	performing an enzyme-linked immunosorbent assay (ELISA) on a saliva	
CC	sample using an anti-serum that is specific for the protein. Saliva	
CC	collection is relatively non-invasive when compared to blood collection	
CC	for serum. Saliva can be centrifuged immediately, whereas blood requires	
CC	clotting time before centrifugation to separate serum. Saliva proteins	
CC	can be assayed by a simple ELISA test, whereas an assay of proteins from	
CC	serum requires a more complicated sandwich type ELISA	
XX		
SO	Sequence 11 AA;	
XX		
Query Match	94.2%; Score 65; DB 7; Length 11;	
Best Local Similarity	100.0%; Pred. No. 0.0013;	
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 LKAMPPTPLM 11	
DB	1 LKAMPPTPLM 11	
XX		
RESULT 6		
AAWS3843		
ID	AAWS3843 standard; peptide; 10 AA.	
XX		
AC	AAWS3843;	
XX		
DT	08-JUL-1998 (first entry)	

DE N-terminus of opossum LTNP.
 XX
 XX LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KM anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KM sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 XX Didelphis virginiana.
 OS
 XX US5744449-A.
 PN
 XX 28-APR-1998.
 PD
 XX 03-JUN-1996; 96US-00657163.
 PF
 XX 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX
 XX (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 PI LIPPS FW, LIPPS BV;
 XX
 XX WPI; 1998-271108/24.
 DR
 XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 XX
 XX Claim 7; Col 11; 11pp; English.
 PS
 XX This sequence represents the peptide of the invention. It is a lethal
 CC toxin neutralising factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 CC
 CC Sequence 10 AA;
 SQ
 Query Match 78.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10
 RESULT 7
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 AC ABB80222;
 XX
 XX 06-NOV-2003 (first entry)
 DE
 XX Synthetic LTNP, LT-10.
 XX
 XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.
 XX
 OS Synthetic.
 XX

XX
 XX WO2003060471-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 14-JAN-2003; 2003WO-US001044.
 PF
 XX 14-JAN-2002; 2002US-00047945.
 PR
 XX (LIPF/) LIPPS B V.
 PA (LIPF/) LIPPS F W.
 XX
 XX LIPPS BV, LIPPS FW;
 PI
 XX WPI; 2003-636703/60.
 DR
 XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 XX Claim 7; Page 3; 24pp; English.
 PS
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 78.3%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10
 RESULT 8
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 AC ABB80227;
 XX
 XX 06-NOV-2003 (first entry)
 DE
 XX Synthetic LTNP, LT-9.
 XX
 XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KM IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KM SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KM saliva; ELISA.
 XX
 OS Synthetic.
 XX
 XX WO2003060471-A2.
 PN
 XX

PD 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003MO-US001044.
 XX
 XX 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI LIPPS BV, LIPPS FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 XX
 PS Claim 7; Page 4; 24pp; English.
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin B (IgB), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgB levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SJS), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's disease, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 CC
 CC
 SQ Sequence 9 AA;
 Query Match 72.5%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPP 9
 DB 1 LKAMDPTPP 9
 RESULT 9
 ADH88053
 ID ADH88053 standard; protein; 137 AA.
 XX
 AC ADH88053;
 XX
 DT 22-APR-2004 (first entry)
 XX
 XX Enterococcus faecalis polypeptide #2533.
 DE Enterococcus faecalis infection; transcription regulatory element;
 XX
 KM Enterococcus faecalis infection; transcription regulatory element;
 KM antibacterial.
 XX
 OS Enterococcus faecalis.
 OS
 PN US6617156-B1.
 XX
 PD 09-SEP-2003.
 XX
 PF 13-AUG-1998; 98US-00134000.
 XX
 PR 15-AUG-1997; 97US-0055778P.
 XX
 PA (DOUC/) DOUCETTE-STAMM L A.

PA (BUSH/) BUSH D.
 XX
 XX Doucette-Stamm LA, Bush D;
 PI
 XX
 DR WPI; 2003-695394/82.
 DR N-PSDB; ADH84648.
 XX
 PT New nucleic acid comprising a sequence encoding an Enterococcus faecalis
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating E. faecalis infection.
 XX
 XX
 PS Disclosure; SEQ ID NO 5938; 193pp; English.
 CC The invention relates to Enterococcus faecalis polynucleotides and
 CC polypeptides. The invention also relates to a recombinant expression
 CC vector comprising a polynucleotide operably linked to a transcription
 CC regulatory element, a cell comprising a recombinant vector, a method for
 CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
 CC a sequence not given in the specification, a recombinant vector
 CC comprising the nucleic acid and a cell comprising the recombinant vector.
 CC The polynucleotides can be used to detect the presence of E. faecalis in
 CC a sample. The sequences are useful for preparing a composition for
 CC diagnosing or treating Enterococcus faecalis infection. This sequence
 CC represents an E. faecalis polypeptide of the invention.
 CC
 CC
 SQ Sequence 137 AA;
 Query Match 65.2%; Score 45; DB 7; Length 137;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DPTPPMWT 12
 DB 85 NPTPLMV 92
 RESULT 10
 ABG22890
 ID ABG22890 standard; protein; 156 AA.
 XX
 AC ABG22890;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22881.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSR-) HYSRQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS87077.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 53249; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptides and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 156 AA;
Query Match 63.8%; Score 44; DB 4; Length 156;
Best Local Similarity 54.5%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLMT 12
DB 141 KAQPPAPPMT 151

RESULT 11
ABG18144
ID ABG18144 standard; protein; 303 AA.

AC ABG18144;
DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #18135.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Dermanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS82331.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 48503; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptides and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 303 AA;

Query Match 63.8%; Score 44; DB 4; Length 303;
Best Local Similarity 54.5%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLMT 12
DB 39 BASDPVPPMT 49

RESULT 12
ABB80228
ID ABB80228 standard; peptide; 8 AA.

AC ABB80228;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNF, LT-8.

KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KM IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KM ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KM SR; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KM Graves' disease; Addison's disease; Hodgkin's disease; depression;
KM saliva; ELISA.

OS Synthetic.
PN WO2003060471-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001044.

PR 14-JAN-2002; 2002US-00047945.

PR 14-JAN-2002; 2002US-00047945.

PA (LIPP/) LIPPS B V.

PI (LIPP/) LIPPS F W.

DR Lippes BV, Lippes FW;

DR WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.

PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTPF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin B (IgB), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

Query Match 62.3%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
 :|:|||||
 Db 1 LKAMDPTP 8

RESULT 13

AAAM79784 standard; protein; 393 AA.

XX AAM79784;
 AC AAM79784;
 XX 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3430.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

PN W0200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSR-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
 PI Xue AJ, Yang Y, Wejrtman T, Goodrich R;

XX MPI: 2001-476283/51.
 DR N-PSDB; AAK52917.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 20; Page 332; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX Sequence 393 AA;

Query Match 62.3%; Score 43; DB 4; Length 393;
 Best Local Similarity 54.5%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLM 11
 :|:|||||
 Db 11 IKLSPPLM 21

RESULT 14

ADM98800 standard; protein; 932 AA.

XX ADM98800;

XX 01-JUL-2004 (first entry)

DE HMW-CoA reductase polypeptide #53.

XX Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;
 KW diterpene synthase; defence toxin; volatile defensive signal;
 KW pollinator attractant; photoprotectant; HMW-CoA reductase; enzyme.
 XX Strongylocentrotus purpuratus.

PN US2004072323-A1.

PD 15-APR-2004.

PF 07-JAN-2002; 2002US-00041018.

PR 05-JAN-2001; 2001US-0259880P.

XX (MATS/) MATSUDA S P T.
 PA (HART/) HART B A.

PI Matsuda SPT, Hart BA,

DR MPI: 2004-373921/35.

PT New unicellular organisms comprising exogenous nucleic acids encoding a
 PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for
 PT producing diterpenes and diterpene precursors.

XX Disclosure; SEQ ID NO 220; 38pp; English.

XX The invention relates to a unicellular organism for producing a diterpene
 CC or diterpene precursor comprising an exogenous nucleic acid sequence
 CC encoding a geranylgeranyl pyrophosphate synthase under the control of a
 CC promoter operable in the organism, and an exogenous nucleic acid sequence
 CC encoding a diterpene synthase under the control of a promoter operable in
 CC the organism. The invention also relates to methods of producing a
 CC diterpene or diterpene precursor and a method of isolating a diterpene
 CC synthase comprising growing several cells in the presence of a
 CC polyaromatic resin to make a cell/resin mixture, where at least one of

CC the cells further comprises at least one isolated and purified nucleic
 CC acid sequence of a yeast expression library, and the expression of the
 CC nucleic acid sequence is regulated by an inducible promoter under
 CC conditions where the expression is induced, filtering the cell/resin
 CC mixture, extracting the cell/resin mixture with alcohol to produce an
 CC organic eluent and analysing the organic eluent by a screening method
 CC including chromatography and/or spectroscopy, to identify the nucleic
 CC acid sequence encoding the diterpene synthase. The unicellular
 CC microorganism is useful as a diterpene or diterpene precursor producing
 CC system. Diterpenes, in plants, serve as defence toxins, volatile
 CC defensive signals, pollinator attractants and photoprotectants. This
 CC sequence represents an Hmg-CoA reductase polypeptide used in the scope of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification but was obtained in electronic format from
 CC USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 932 AA;
 Query Match 62.3%; Score 43; DB 8; Length 932;
 Best Local Similarity 70.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KAMDPTPLW 11
 DB 298 KKIDPTPLW 307
 RESULT 15
 AAR56496
 ID AAR56496 standard; protein; 1189 AA.
 XX
 AC AAR56496;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAR-1995 (first entry)
 XX
 DE TATA-binding protein-associated factor dTAFI50.
 XX
 KW TATA-binding protein associated factor; dTAFI50; screening; diagnostic;
 KW therapeutic; gene transcription regulation.
 XX
 OS Drosophila.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 923
 FT /note= "Val or Leu"
 FT Misc-difference 1106
 FT /note= "Arg, Pro or His"
 FT Misc-difference 1172
 FT /note= "STOP"
 FT Misc-difference 1176
 FT /note= "STOP"
 XX
 PN WO9417087-A1.
 XX
 PD 04-AUG-1994.
 XX
 PF 28-JAN-1994; 94WO-US001114.
 XX
 PR 28-JAN-1993; 93US-00013412.
 PR 30-JUN-1993; 93US-00087119.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tjian R, Comai L, Dynlacht BD, Hoey T, Ruppert S, Tanese N;
 PI Wang E, Weinzierl ROJ;
 XX
 DR WPI; 1994-264019/32.
 DR N-PSDB; AAG70733.
 XX
 PT TATA-binding protein associated protein factors - and corresponding
 PT nucleotide sequence and deriv. antibodies, useful in screening,
 PT diagnostics and therapeutics.

XX
 PS Disclosure; Page 156; 180pp; English.
 XX
 CC The TATA-binding protein associated factor hTAFI50 (including specific
 CC antibodies and fusion products) are used in drug screening, diagnostics
 CC and therapeutics. They are used in the development of specific
 CC biochemical assays for screening compounds that agonise or antagonise
 CC selected transcription factors involved in regulating gene expression
 CC associated with human pathology. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 1189 AA;
 Query Match 62.3%; Score 43; DB 2; Length 1189;
 Best Local Similarity 66.7%; Pred. No. 4.2e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLW 12
 DB 589 LSAMDSPVLW 600
 Search completed: January 6, 2005, 10:22:48
 Job time : 96.3513 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:23:04 ; Search time 81.0811 Seconds
(without alignments)
53.365 Million cell updates/sec

Title: US-10-047-945-4
Perfect score: 69
Sequence: 1 LKAMDPTPLMT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubppaa/US09C_NEW_PUB.pep.*
- 12: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	US-10-047-945-4	Sequence 4, App11
2	69	100.0	15	US-10-047-945-2	Sequence 2, App11
3	65	94.2	11	US-10-047-945-5	Sequence 5, App11
4	54	78.3	10	US-10-047-945-1	Sequence 1, App11
5	50	72.5	9	US-10-047-945-6	Sequence 6, App11
6	44	63.8	106	US-10-424-599-255201	Sequence 255201,
7	44	63.8	124	US-10-424-599-151167	Sequence 151167,
8	44	63.8	144	US-10-424-599-205702	Sequence 205702,
9	43	62.3	8	US-10-047-945-7	Sequence 7, App11
10	43	62.3	115	US-10-425-115-322493	Sequence 322493,
11	43	62.3	129	US-10-437-963-168841	Sequence 168841,
12	43	62.3	932	US-10-041-018-220	Sequence 220, App
13	42	60.9	82	US-10-437-963-128480	Sequence 128480,

14	42	60.9	1336	US-10-177-293-228	Sequence 228, App
15	41	59.4	37	US-09-864-761-45321	Sequence 45321, A
16	41	59.4	41	US-10-424-599-173148	Sequence 173148,
17	41	59.4	64	US-09-864-761-39999	Sequence 39999, A
18	41	59.4	68	US-10-425-115-251177	Sequence 251177,
19	41	59.4	80	US-10-424-599-253125	Sequence 253125,
20	41	59.4	86	US-10-424-599-220724	Sequence 220724,
21	41	59.4	87	US-10-424-599-179202	Sequence 179202,
22	41	59.4	148	US-10-437-963-133945	Sequence 133945,
23	41	59.4	151	US-10-425-115-327173	Sequence 327173,
24	41	59.4	176	US-10-097-065-274	Sequence 274, App
25	41	59.4	212	US-09-889-722-387	Sequence 387, App
26	41	59.4	212	US-09-889-723-387	Sequence 387, App
27	41	59.4	212	US-09-889-729-387	Sequence 387, App
28	41	59.4	212	US-09-889-727-387	Sequence 387, App
29	41	59.4	212	US-09-889-731-387	Sequence 387, App
30	41	59.4	212	US-09-889-732-387	Sequence 387, App
31	41	59.4	212	US-09-891-073-387	Sequence 387, App
32	41	59.4	212	US-09-890-442-387	Sequence 387, App
33	41	59.4	212	US-09-891-163-387	Sequence 387, App
34	41	59.4	212	US-09-893-604-387	Sequence 387, App
35	41	59.4	212	US-09-890-456-387	Sequence 387, App
36	41	59.4	212	US-09-889-721-387	Sequence 387, App
37	41	59.4	212	US-09-889-721-387	Sequence 387, App
38	41	59.4	212	US-09-889-293A-387	Sequence 387, App
39	41	59.4	212	US-09-889-735-387	Sequence 387, App
40	41	59.4	212	US-09-890-444-387	Sequence 387, App
41	41	59.4	212	US-09-891-181-387	Sequence 387, App
42	41	59.4	212	US-09-889-730-387	Sequence 387, App
43	41	59.4	212	US-09-890-436-387	Sequence 387, App
44	41	59.4	212	US-09-893-687-387	Sequence 387, App
45	41	59.4	212	US-09-893-687-387	Sequence 387, App

ALIGNMENTS

RESULT 1
US-10-047-945-4 Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FPLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMT 12
|||||
Db 1 LKAMDPTPLMT 12

RESULT 2

US-10-047-945-2
; Publication 2, Application US/10047945
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINTIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)IMPLICATED DISORDERS
; FILE REFERENCE: FMI/PAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
US-10-047-945-2 SERUM

Query Match 100.0%; Score 69; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPLWI 12
DB 1 LKAMDPTPTPLWI 12

RESULT 3
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINTIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)IMPLICATED DISORDERS
; FILE REFERENCE: FMI/PAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 94.2%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPLW 11
DB 1 LKAMDPTPTPLW 11

RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945

Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINTIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)IMPLICATED DISORDERS
; FILE REFERENCE: FMI/PAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
US-10-047-945-1 SERUM

Query Match 78.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTPL 10
DB 1 LKAMDPTPTPL 10

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINTIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IG)IMPLICATED DISORDERS
; FILE REFERENCE: FMI/PAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 72.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPTP 9
DB 1 LKAMDPTPTP 9

RESULT 6
US-10-424-589-255201
; Sequence 255201, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255201
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201

Query Match
Best Local Similarity 63.8%; Score 44; DB 15; Length 106;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRPPLMW 12
DB 92 PRPPLMW 98

RESULT 7
US-10-424-599-151167
; Sequence 151167, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151167
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107527C.1.pep
US-10-424-599-151167

Query Match
Best Local Similarity 63.8%; Score 44; DB 15; Length 124;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPLMW 12
DB 96 DPTPLMW 103

RESULT 8
US-10-424-599-205702
; Sequence 205702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205702
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(144)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27777C.1.pep
US-10-424-599-205702

Query Match
Best Local Similarity 63.8%; Score 44; DB 15; Length 144;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRPPLMW 12
DB 28 PRPPLMW 34

RESULT 9
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; FILE REFERENCE: PMLPRT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match
Best Local Similarity 62.3%; Score 43; DB 14; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 10
US-10-425-115-322493
; Sequence 322493, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 322493
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LENGTH: 115
TYPE: PRT
ORGANISM: Zea mays
FEATURES:
OTHER INFORMATION: Clone ID: MRT4577_57178C.1.pep
US-10-425-115-322493

Query Match 62.3%; Score 43; DB 17; Length 115;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPPPLW 12
DB 43 DPTPPPLW 50

RESULT 11
US-10-437-963-168841
Sequence 168841, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168841
LENGTH: 129
TYPE: PRT
ORGANISM: Oryza sativa
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT4530_67316C.1.pep
US-10-437-963-168841

Query Match 62.3%; Score 43; DB 16; Length 129;
Best Local Similarity 63.6%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMPPTPLW 11
DB 84 LKAMPPTPLW 94

RESULT 12
US-10-041-018-220
Sequence 220, Application US/10041018
Publication No. US20040072323A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.1
SEQ ID NO 220
LENGTH: 932
TYPE: PRT
ORGANISM: Strongylocentrotus purpuratus
US-10-041-018-220

Query Match 62.3%; Score 43; DB 15; Length 932;
Best Local Similarity 70.0%; Pred. No. 5,1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMPPTPLW 11
DB 298 KKIDPTPLW 307

RESULT 13
US-10-437-963-128480
Sequence 128480, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 128480
LENGTH: 82
TYPE: PRT
ORGANISM: Oryza sativa
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT4530_30829C.1.pep
US-10-437-963-128480

Query Match 60.9%; Score 42; DB 16; Length 82;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPPPLW 12
DB 75 EPTPPCWI 82

RESULT 14
US-10-177-293-228
Sequence 228, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatc, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavaipui, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Baat Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21

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;; PRIOR APPLICATION NUMBER: US 60/239,887
;; PRIOR FILING DATE: 2001-06-21
;; PRIOR APPLICATION NUMBER: US 60/301,572
;; PRIOR FILING DATE: 2001-06-27
;; PRIOR APPLICATION NUMBER: US 60/306,501
;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: US 60/325,002
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US 60/362,585
;; PRIOR FILING DATE: 2002-03-05
;; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 506
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 228
;; LENGTH: 1336
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-177-293-228
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Query Match          60.9%; Score 42; DB 14; Length 1336;
Best Local Similarity 77.8%; Pred. NO. 1e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      4 MDPTPLMT 12
DB      34 MDPOPBLMT 42
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RESULT 15
US-09-864-761-45321
; Sequence 45321, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 45321
;; LENGTH: 37
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL133458.11
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
;; OTHER INFORMATION: SWISSPROT HIT: O53951, EVALU6 6.40e+00
;; OTHER INFORMATION: EST_HUMAN HIT: AI986481.1, EVALU6 6.00e-16
US-09-864-761-45321
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Query Match          59.4%; Score 41; DB 9; Length 37;
Best Local Similarity 54.5%; Pred. NO. 50;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY      2 KAMDPTPLMT 12
DB      5 KSMGPAPPRM 15
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Job time : 82.0811 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:51, Search time 24.3243 Seconds
(without alignments)
32.717 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMPTPLMT 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/backfill1a1.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	15	1 US-08-310-340A-1	Sequence 1, Appl
2	69	100.0	15	1 US-08-657-163A-1	Sequence 1, Appl
3	54	78.3	10	1 US-08-657-163A-2	Sequence 2, Appl
4	45	65.2	137	4 US-09-134-000C-5938	Sequence 5938, Ap
5	43	62.3	1213	1 US-08-188-582-20	Sequence 20, Appl
6	43	62.3	1213	1 US-08-646-715-20	Sequence 20, Appl
7	41	59.4	212	4 US-10-140-002-482	Sequence 482, Ap
8	41	59.4	253	4 US-09-270-67-43223	Sequence 43223, A
9	40	58.0	198	4 US-09-270-767-57545	Sequence 57545, A
10	40	58.0	360	4 US-09-270-767-42265	Sequence 42265, A
11	39	56.5	206	2 US-08-477-396A-18	Sequence 18, Appl
12	39	56.5	210	4 US-09-270-767-45215	Sequence 45215, A
13	38	55.1	267	2 US-07-857-224B-42	Sequence 42, Appl
14	38	55.1	1740	4 US-09-377-285B-40	Sequence 40, Appl
15	37	53.6	15	3 US-08-602-999A-444	Sequence 444, App
16	37	53.6	15	4 US-09-500-124-444	Sequence 444, App
17	37	53.6	78	4 US-09-248-796A-21988	Sequence 21988, A
18	37	53.6	87	4 US-09-270-767-41296	Sequence 41296, A
19	37	53.6	87	4 US-09-270-767-56512	Sequence 56512, A
20	37	53.6	196	4 US-09-252-991A-26963	Sequence 26963, A
21	37	53.6	207	4 US-09-328-352-6054	Sequence 6054, Ap
22	37	53.6	210	4 US-09-071-035-232	Sequence 232, App
23	37	53.6	226	4 US-09-071-035-230	Sequence 230, App
24	37	53.6	261	4 US-09-270-767-43480	Sequence 43480, A
25	37	53.6	291	4 US-09-134-000C-6676	Sequence 6676, Ap
26	37	53.6	306	4 US-09-134-000C-6583	Sequence 6583, Ap
27	37	53.6	387	4 US-09-252-991A-30473	Sequence 30473, A

28	37	53.6	427	4 US-08-311-731A-216	Sequence 216, App
29	37	53.6	502	4 US-09-540-236-3413	Sequence 3413, Ap
30	37	53.6	528	4 US-09-270-767-42895	Sequence 42895, A
31	37	53.6	3170	2 US-07-642-734C-5	Sequence 5, Appl
32	37	53.6	3170	3 US-08-439-009A-5	Sequence 5, Appl
33	37	53.6	4928	3 US-09-036-987A-5	Sequence 5, Appl
34	37	53.6	4928	3 US-09-370-700-5	Sequence 5, Appl
35	37	53.6	4928	4 US-09-603-207-5	Sequence 5, Appl
36	36	52.2	119	4 US-09-248-796A-25521	Sequence 25521, A
37	36	52.2	200	4 US-09-252-991A-27890	Sequence 27890, A
38	36	52.2	230	3 US-09-187-789-7	Sequence 7, Appl
39	36	52.2	230	3 US-09-989-903-7	Sequence 7, Appl
40	36	52.2	280	3 US-09-247-155-178	Sequence 178, App
41	36	52.2	323	4 US-09-489-039A-13655	Sequence 13655, A
42	36	52.2	338	4 US-09-248-796A-15934	Sequence 15934, A
43	36	52.2	338	4 US-09-248-796A-20624	Sequence 20624, A
44	36	52.2	409	4 US-09-270-767-45869	Sequence 45869, A
45	36	52.2	498	4 US-09-270-767-42848	Sequence 42848, A

ALIGNMENTS

RESULT 1
US-08-310-340A-1
Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 69; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMI 12
DB 1 LKAMDPTPLMI 12

RESULT 2

US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1

Query Match 100.0%; Score 69; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMI 12
DB 1 LKAMDPTPLMI 12

RESULT 3

US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 78.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
DB 1 LKAMDPTPL 10

RESULT 4
US-09-134-000C-5938
Sequence 5938, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FASCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5938
LENGTH: 137
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5938

Query Match 65.2%; Score 45; DB 4; Length 137;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPLMI 12
DB 85 NPTPLMV 92

RESULT 5
US-08-188-582-20
Sequence 20, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko

APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osgan, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/ALT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-582-20

Query Match 62.3%; Score 43; DB 1; Length 1213;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMI 12
DB 620 LSHMDSPLVMI 631

RESULT 6
US-08-646-715-20
Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AUT/PAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277239
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-715-20

Query Match 62.3%; Score 43; DB 1; Length 1213;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKMDPTPLMI 12
DB 620 LSAMDSPVLMI 631

RESULT 7
US-10-140-002-482
Sequence 482, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C5
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 482
LENGTH: 212
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-002-482

Query Match 59.4%; Score 41; DB 4; Length 212;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLMI 12

DB 136 MDSPVPMI 144

RESULT 8
US-09-270-767-43223
Sequence 43223, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43223
LENGTH: 253
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43223

Query Match 59.4%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPL 10
DB 43 MDPTPL 49

RESULT 9
US-09-270-767-57545
Sequence 57545, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57545
LENGTH: 198
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57545

Query Match 58.0%; Score 40; DB 4; Length 198;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKMDPTPLMI 11
DB 70 IKAVSPSPNLM 80

RESULT 10
US-09-270-767-42265
Sequence 42265, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42265
LENGTH: 360
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42265

Query Match 58.0%; Score 40; DB 4; Length 360;
Best Local Similarity 54.5%; Pred. No. 84;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMPPTPLM 11
DB 70 IKAVSPSPNLM 80

RESULT 11
US-08-477-396A-18
Sequence 18, Application US/08477396A
Patent No. 5872235
GENERAL INFORMATION:
APPLICANT: Chen, Ian Bo
APPLICANT: Bao, Shideng
APPLICANT: Liu, Yuan
TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
TITLE OF INVENTION: ISOLATING SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,396A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,488
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: US 08/448,388
FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12502
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DPCI-333BX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-477-396A-18
Query Match 56.5%; Score 39; DB 2; Length 206;

Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLMT 12
DB 82 LDGNPPLMT 90

RESULT 12
US-09-270-767-45215
Sequence 45215, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45215
LENGTH: 210
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-45215

Query Match 56.5%; Score 39; DB 4; Length 210;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMPPTPLM 11
DB 134 KSDDPTNPLM 143

RESULT 13
US-07-857-224B-42
Sequence 42, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TYPE: none
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae

```
/ FEATURE: Protein kinase; Table 8 Column 48
/ PUBLICATION INFORMATION:
/ AUTHORS:
/   AUTHORS: Hanks, S. K.
/   AUTHORS: Quint, A. M.
/   AUTHORS: Hunter, T.
/   TITLE: The protein kinase family
/   JOURNAL: Science
/   VOLUME: 241
/   PAGES: 42-52
/   DATE: 1988
/ US-07-857-224B-42

Query Match      55.1%; Score 38; DB 2; Length 267;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
   |||||
   :|||:
Db 31 LKVDPTPEL 40

RESULT 14
US-09-377-285B-40
/ Sequence 40, Application US/09377285B
/ Patent No. 6720175
/ GENERAL INFORMATION:
/ APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
/ APPLICANT: MORLEY, Paul
/ APPLICANT: TU, Jian
/ APPLICANT: XIAO, Bo
/ APPLICANT: LEAHY, Daniel
/ APPLICANT: BENEFEN, Jutta
/ APPLICANT: LANAHAN, Anthony
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
/ FILE REFERENCE: JHU1580-4
/ CURRENT APPLICATION NUMBER: US/09/377,285B
/ PRIOR FILING DATE: 1999-08-18
/ PRIOR APPLICATION NUMBER: US 60/138,426
/ PRIOR FILING DATE: 1999-06-10
/ PRIOR APPLICATION NUMBER: US 60/138,493
/ PRIOR FILING DATE: 1999-06-10
/ PRIOR APPLICATION NUMBER: US 60/138,494
/ PRIOR FILING DATE: 1999-06-10
/ PRIOR APPLICATION NUMBER: US 60/097,334
/ PRIOR FILING DATE: 1998-08-18
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 40
/ LENGTH: 1740
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ US-09-377-285B-40

Query Match      55.1%; Score 38; DB 4; Length 1740;
Best Local Similarity 62.5%; Pred. No. 9.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPTPL 11
   |||||
   :|||:
Db 26 LDPTAPV 33

RESULT 15
US-08-602-999A-444
/ Sequence 444, Application US/08602999A
/ Patent No. 6184205
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
```

```
/ APPLICANT: FOWLES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennile & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ - CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999A
/ FILING DATE: 16-FEB-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mirock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 444:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-602-999A-444

Query Match      53.6%; Score 37; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
   |||||
   :|||:
Db 5 RALPTPL 13
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Search completed: January 6, 2005, 10:25:07
Job time : 25.3243 secs